

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCG
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG
CTGCTGCCGCCCCGCGCCGGAGGCCGCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT
GGTGGACAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCCGGAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA
GGGCGACGGGTCTGCCGGTGCCACATGGGGTACCAGGGCCCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACAGTGCAGAGAGTGTGACTCCAGCTGTGTG
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
AAAAGTGTACAATACTCCAGGGAGCTACGTCTGTGTGTGTCTTGACGGCTTCGAAGAAACG
GAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT
GCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTACCCTTTAAATTATTCAGAAGGATGTCC
CGTGGAAGTGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTCCCTTAAACAGCTGCATTTCTTGTTGTTCTTA
AACAGACTTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCA
TCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAACTC
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTCGGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACTTGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCAGGCTCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTTT

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FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEKTL SKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFVCVTKLVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHS ICTACDESKTCSGLTNRDCGECEVGWVLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
CVRKNENCYNTPGSYVCVCPDGFEEEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

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CGCCATGGCCCAACTTGTTATTGCAGCTTATAATG

FIGURE 4

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><subunit 1 of 1, 379 aa, 0 stop

><MW: 41528, pI: 7.97, NX(S/T): 2

MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESELYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMIPAIPVNIHSMNFTWQAAGQAEYFYEFSLSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGC
RNGGFCNERRICEPCDGFHGHPCHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNNGGTCFYPGKICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHPTPSLKKAERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

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FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTTCGCAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG
CCCCAGCCCACACCTTCACCAGGGCCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCCAGCAGGGTCGTGGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCTTCGGCGTGCCACCCCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA
TCCAGTCTTGGAACGTACTGGGACAACGTGAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTTCTGGGGCATGACCCTGGATTGAGGGCATTTCGCTACCGCCTGGGCACCA
TCCGCCCATCTTCCTCGGTTCATGAACATGCATGAAATTTATACAGTGCTGAACCCAGGGGAG
GTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTTCATGAGCCTCTTGA
CCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCTGTCTGTGCGCCCAAGAACCTGCTGTCTTGTGAC
ACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTTCGGGGCAAGCGCCAGGCCACTGCC
CACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCCTGGGGCC
CAGCCTGGGGCGAGAGGGGGCCACTTCCGCATCGTGCGCGGCGTCAATGAGTGCGACATCGAG
AGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTTCATCACTGAGGCTG
CGGGCACCACGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGGCCCCAATG
GGGCGGTGACCCAGCCTCGCCCGACAGAGCCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAAT
CCCGGCGCGGGTTCCGCTGACGCAGCGCCCCGCCTGGGAGCCGCGGGCAGGCGAGACTGGCG
GAGCCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCAG
ATCCAGGCCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG
TTGCCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA
AGTGACCCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACCACACCTGGC
TAATTTTTGTATTTTTTTGTAAAGAGGGGGGTCTCACTGTGTTGCCCAGGCTGGTTTCGAAC
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTGCTGGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAAA
TAAAACCAAAGTATTGATAAAAAAAA

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FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

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FIGURE 7

AGGCTCCTTGGCCCTTTTTCCACAGCAAGCTTNTGCNATCCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCCCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

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FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTCCTGGTTCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCCTGACCCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCCCTCCAACCCTCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCCTCACATTCGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

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FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLLPSSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSSDT
DPPADGPSNPLCCCFHGPFAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

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FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCGCCTGCTGCCCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTCACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTG
CGTGTTACGGAGATCGTGCTGGAGAACAACTATACGGCCTTCCAGAACGCCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCGGCAGGGGCGGCCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGCGCGAGGCCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCACGC
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGGACCAAGCGCACAC
GGCGGCCCCAGCCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCCCTGGGCGCCTCCC
CACCCCTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCTGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTG
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTCAACCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTCAGCGACTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGTCCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTTGTTTGTTTGTTTGTTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCCCACCCCAACTCCCAGCCC
CGGAATAAAACCATTTTCCTGC

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FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNRGKLGKPSGKSKDCVFTEIVLENNYTAFQONARHEGWFMATRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEFVGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

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FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
GACAGCAGCAAAGAGGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
CATTTTGATTTTGCTGTTTATTTTTTTTTTTCTTTTCTTTTCCCACCACATTGTATTTTAT
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCCAGCCATGGGGCTTTTTTCCT
GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC
CTAGTGTGTGCCGCTGCGACAGGAACCTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC
TGGATTTCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTTGCAGGAAAAC
AATATTACAGACCATTTACGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACGGGGCCTTCCGGGAGGGCTATTAGCC
TCAAATTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGGCCTTCCAGAA
TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCC
CACCCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACCAGAT
AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC
ACTGCTCGGAATAACCCTTGTTTTGTGACTGCAGTATTAAATGGGTACAGAAATGGCTCAA
ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCCTGAACAAGTCCGGG
GGATGGCCGTGAGGGAATTAAATATGAATCTTTTGTCTGTCCACCACGACCCCCGGCCTG
CCTCTCTTCACCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTAT
TCCAAACCCTAGCAGAAGCTACACGCCTCCAACCTCCTACCACATCGAAACTTCCCACGATTC
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC
CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTACCCTGATGGCATA
CAAACCTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTGTTCAGAGGC
CACCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT
GTGCTGGTGGTCTTGCTCAGCGTCTTTTGTGCTGGCATATGCACAAAAGGGGCGCTACACCTC
CCAGAAGTGGAAATAACAACGGGGGCCGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTTTCAGATCGTCTCCTTAAATAACGAT
CAACTCCTTAAAGGAGATTTTCAGACTGCAGCCATTTACACCCCAAATGGGGGCATTAATTA
CACAGACTGCCATATCCCCAACAACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC
ACTGCCATACGTAAGCAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT
TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG
CTATCTTTCTATTTCAAGTTAATTACAAACAGTTTTTGTAACCTTTGCTTTTTTAAATCTT

FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLVYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLLDDNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMVRELNMNLLSCPTTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPDWDGRERVTPPISERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNRYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

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FIGURE 14

ACTTGGAGCAAGCGGCGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCCTCGCCTCCCACGAGCG
ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCCCTGCC
TCGCTTCCAGGCGCGGCGGCTGCAGCCTTGCCCCCTCTTGCTCGCCTTGAAAATGGAAAAGATGCTCGCAGGCT
GCTTTCTGCTGATCCTCGGACAGATCGTCCCTCCCTGCCGAGGCCAGGTACGTGGGAGGTCCATCT
CTAGGGGCGAGACACGCTCGGACCCACCCGAGACGGCCCTTCTGGAGAGTTCTGTGAGAACAAGCGGGCAGACC
TGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA
TCTTGCAATTCTTGGACATTGGTCTGTATGTCAACCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGAATG
AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGTGTCAAGAGGATGCGGCATCTGTCCACGG
GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCCGGCCCTGA
GGGAGAATGTGCCACGGGTGATGATCGTGCAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGCTGCTA
AGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCGAGGTAGACTTCAACACCTTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGTCTTCTTGTGGCCAATTTAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGCACGGCCCATGTGTCAGCACCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTG
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT
GTGCCATGGAGGACCACAACTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAAAACACGGATGTGAAC
ATGAGTGTGTAAATGCTGATGGCTCCTACCTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAA
CGTGACAAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCGAGTGGACCACTGTGCAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCTTCGTCTGCCAGTGCTCAGAAGGCTTCC
TCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGGATTACTGCCTGCTGAGTGACCATGGTTGTGAATACTCCT
GTGTCAACATGGACAGATCCTTTGCCTGTGAGTGTCTGAGGGACAGTGCTCCGAGCGATGGGAAGACGTGTG
CAAAATTTGACTCTTGTGCTCTGGGGGACACGGTTGTGTAACATTCTGTGTGAAGCAGTGAAGATTCTGTTGTG
GCCAGTGCTTTGAAGGTTATATACTCCGTGAAGATGGAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTATAG
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACAGTGCAGTGCTTGGAGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAATCAACCCACCATGGCTGCCAACACATTTGTGTGA
ATAATGGGAATTCCTACATCTGCAATGTCTGAGGGGATTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAAT
GCACTGAAGGCCCAATTGACCTGGTCTTTGTGATCGATGGATGCAAGAGTCTTGGAGAAGAGAATTTTGGAGTGC
TGAAGCAGTTTGTCACTGGAATTATAGATTCTCTTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGT
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAACTTCAACTCAGCCAAAGACATGAAAAAAGCCGTGGCCC
ACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAGTTTACCCAAG
GAGAAGGGGCCAGGCCCCCTTCCACAAGGGTGCCAGAGCAGCCATTGTGTTACCGACGGACGGGCTCAGGATG
ACGCTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG
AGGAGGAACACAAAGAGATTGCCTCTGAGCCCAAAACAAGCATCTCTTCTATGCCGAAGACTTCAACCAATGG
ATGAGATAAGTGA AAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAAC TGCCAAAACGGTCCAACAGCCAACAGAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT
CCTGTTCTAATTTTGCAGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTT
CCCATTCAACAAAACCTTCAAGGAAGCCCTTTGGAAGAAAAACCGATCAATGCAATGTGAAAACCTTATAATGT
TCCAGAACCCTTGCAACGAAGAAGTAAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC
TGGA AAATCGCCTGAGATACAGATGAAGATTAGAAAATCGCGACACATTTGTAGTCATTGTATCACGGATTACAAT
GAACGCAGTGACAGAGCCCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAACAATCAGTACTGA
GAAACCTGGTTTGCCACAGAACAAAGACAAGAAGTATACACTA ACTTGTATAAATTTATCTAGGAAAAAATCCT
TCAGAATTCTAAGATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAATATACTGTGGACAC
AACTTGCTTCTGCCTCATCCTGCCTTAGTGTGCAATCTCATTTGACTATACGATAAAGTTTGCACAGTCTTACTT
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTGTACTGGACTTTACCTTGATATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTTATACAATATTTAAATTCACCACTTCAG

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FIGURE 15

MEKMLAGCFLILGQIVLLPAEARERSRGRSISRGRHARTHPQTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV
KRMRLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKP GC
EHECVNMEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTC SRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTC AKLDSCALGDHGCE
HSCVSSSEDSFVCQC FEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLA
EDGKRCRRKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEELQEIASPTNKHLYAEDFSTMDIEISEKLKKGICEALEDSDGRQDS
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEFNLLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTTGTTCTTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTTCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCAGCGTGGTACACCTTGACGGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCCTCTGTCACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAT
TGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCCACGACAGAT
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCCTGCCAGAGTCAAGCTGGCTCTCTGGTATGATGAC
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAATAACTAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAAGATACATAA
TGTTTGTATGAAAAA

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FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGCVSS
SQPWEVVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKGSGPY
SCSVNVQDKQGKSRGHSIKTLELNLVLPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQ
WDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL
SSVTSARALRPPHGPFRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

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FIGURE 19

MKRLPLLVFSTLLNCSYTONCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSIYCMCVPGFRSSSNQDRFITNDGTVCIENVNANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL
SNSTLTETVKTNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFQKTTEFDT
NSTDIALKVFFFDSDYNMKHIHPHMNMGDYINIFPKRKAAYDSNGNVAVAFLLYYKSIGPLLS
SSDNFLLKPQNYDNSEEEERVISVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF
WNYSPTMTNGSWSSSEGCELTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSTIAGL
LHYFFLAFAWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSALGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT
TGGTCCCTTTGCTTTTCATCATCTGACAACTTCTTATTGAAACCTCAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA
GGAGTCTATGTGGCATTFTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

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FIGURE 21

GCTCCAGCCAAGAACCTCGGGGCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCGGCTGGGA
CAAGAAGCCGCGCCTGCCTGCCCGGGCCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGTCTTGGGCACCTACCCGTGGGGCCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCCGAG
CCGCGCGCCGTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCATCGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCC
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCGTGGACTGCGCGCGGGGC
CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
CGTGACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTTGGGCTTGTCACCGGACTGGAGGCCGTGAGGAGTCCCAGCTTTGAGAAGTAACT
GAGACCATGCCCGGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
GTTGTACATATTAGAGTTTTCCATTGGCAGTGCCAGTTTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCCAGCTGCTGCCTGGGCCCCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
TCACTTCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTAGGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCACCAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAATTCCCC
CTGAGGCCAGTTCTGTGATGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGTCACCTGC
TTCCATCTCCCAGCCCCACCAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGGCCT
CCCAGGCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC
CCTTTCCCCAGCACTTGGTTTTTCAACATGATATTTATGAGTAATTTATTTTGATATGTACA
TCTCTTATTTTCTTACATTATTTATGCCCCAAATTATATTTATGTATGTAAGTGAGGTTTG
TTTTGTATATTAAAATGGAGTTTGTTTGT

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FIGURE 22

MRS GCVVHVWILAGLWLA VAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAV ALRTVAIKGVH SVRYLCMGADGKMQGLLQYSEEDCA FEE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

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FIGURE 23

CCCAGAAGTTCAAGGGCCCCCGGCTCCTGCGCTCCTGCCGCCGGGACCCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTGCCTTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA
AGAAGACTGTTTCCTCCAGATTAGAGTGGAAGAACTGGGTCCGAGTGTCTCCTTTGTCTAC
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATAACAATGAATACAAAACTGGAAGT
CTGCAATTTAATACTGTTTCCAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATTC
TGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAA
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGG
CCGCGGCGGGCGGATCACGAGGTCAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGGTAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATA
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

FIGURE 24

MARRSRHRLLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQONLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNVSGYRRCPGKRMQVDDLNIISGIIAAVVVVA
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWCAAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

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FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCCTGGCAT
CATGCTGCTATTCTCTGCAATACTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTGGACAATG
CAATTGTGGCACTGGCACTTATTTTCAGTGAAGAAAACTTTGTGGTTCTATGGCATTTCATCA
TTTGACAAATGCAAGCATCTTCCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTG
TGGAATCCTTAAGGGCCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCAGATTGCC
AGCTAACACACAGATTCTTCTCCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAG
ACTTTCAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTCACCAAT
ATTAATGTAAAAAAGATGCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAACAACTTACTGA
ACTGCCTGAAAAATGTCTGTCCGAAGTGAAGCACTTACAAGAACTCTATATTAATCACAAC
TGCTTTCTACAATTTACCTGGAGCCTTTATTGGCCTACATAATCTTCTTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAGAGAT
TCTGATGATTGGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTTAAGCCTCTTATCA
ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTTTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTCTTCAAAAAGTTGTAAATCTCAAATTTTTGGATCTAAATAAAAATCCTATTAATAGAA
TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGATAAATAATATGCCT
GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC
TACTAACAAACCCTAGATTGTCTTACATTACCCCCAATGCATTTTTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATAACAGTAACCCCATCAGGTGTGACTGTGTGCATCCGTTG
GATGAACATGAACAAAACCAACATTCGATTTCATGGAGCCAGATTCAGTGTGCTGCTGGACC
CACCTGAATTCGAAGGTGAGAATGTTTCGGCAAGTGCATTTTCAGGGACATGATGGAAATTTGT
CTCCCTCTTATAGCTCCTGAGAGCTTTCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT
TTCCTTTCACTGTAGAGCTACTGCAGAACCACAGCCTGAAATCTACTGGATAACACCTTCTG
GTCAAAAACCTTGCCTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA
GATATAAATGGCGTAACTCCCAAAGAAGGGGGTTTATATACTTGTATAGCAACTAACCTAGT
TGCGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG
GCTCTTTGAATATTAAAATAAGAGATATTGAGGCAATTCAGTTTTTGGTGTCTTGGAAAGCA
AGTTCTAAAATTTCTCAAATCTAGTGTTAAATGGACAGCCTTTGTCAAGACTGAAAATTTCTCA
TGCTGCGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAAATTTGTATTGATATTCCCACCATCTATCAGAAAAACAGAAAAAA
TGTGTAAATGTCACCACCAAGGTTTGCACCCTGATCAAAAAGAGTATGAAAAGAATAATAC
CACAACACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA
AGAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCTT
AAAAACCACCAAGGAAACCTACTCCAAAATGAAC

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FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLLQTNNAKIEYSTDFVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTTELPEKCLSELNLQELYINHNLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVNLKFLDLNKNPINRIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLDP
LRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEISIHSPNIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGNVRQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRTAEAPQPEIYWITPSGQKLLPNTLTDFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFFV
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPMNCDGGHSYVRNYLQKPTFALGELYPPPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

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FIGURE 27

GCCCGGGACTGGCGCAAGGTGCCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTAG
CTGCAGCCTTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTA
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTTAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGACAGACTCTGGACTTGTCGGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTTGTAACTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTTGGCTGGTTCATATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
GATGCCCCGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTTGCGATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA
ACTTTGTATTTTCAAGTTTTTTTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACA
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT
AATTTAAAAGCAAATAAAAGCTTAACTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

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FIGURE 28

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMCPKGCLCSSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICHTSVLDEHAGRPFL
NAANDADLCNLPKKTDDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

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FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCGAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCT
GGGCTCAGTGCTGTGAGGCTCGGCCACGGGCTGCCCCGCCCGCTGCGAGTGCTCCGCCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACC GCATCAAAACGCTCAACCAGGACGAGTTCGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCCGGCG
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGAT
CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCTCACC GCGCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGCACGGCCT
CATCGTCTTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCCTCAACCTCTCCTACAACCCCATCA
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGCTCAA
TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCCTGTGGGTGTTCCGG
CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCCCGAGTTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCAACTACTTCACCTGCCGCCGCG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACACGGTGCAGTTT
GTGTGCCGGGCCGATGGCGACCCGCGCCCGCCATCCTCTGGCTCTCACCCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGAC
TCCATGCCCCGCCACCTGCATGTGCGCAGCTACTCGCCCCGACTGGCCCCATCAGCCCAACAA
GACCTTCGCTTTCATCTCCAACCAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG
TGCCTTTCCTTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC
CTGGGCGTCGTCTCTTCTGCCTGGTGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC
AAAGCACAAATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCCGGGGCGGGGGGCAGGGACCCCCG
GGCGGCCGGGCAGGGGAAGGGGCTGGTGCACACCTGCTCACTCTCCAGTCTTCCCACCTC
CTCCCTACCCTTCTACACACGTTCTCTTCTCCCTCCCGCCTCCGTCCCCTGCTGCCCCCG
CCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCCAGACCTGGGGACCCCA
CCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACTTGGGTTTCAATAATTATGGATTTT
TATGAAAACCTGAAATAATAAAAAAGAGAAAAAACTAAAAA

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FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELELNENIVSAVEPGAFFNNLFLNLRTL
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA
FSGNLNLEQLTLEKCNLTSTIPTEALSHLHGLIVLRLRHLNINAI RDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRLFLNLSYNPISTIEGSM LHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTLEESVFHSGNLET LILDSNPLA
CDCRLLWVFRRRWRLNFRNQOPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARI DRKAQQV
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGR LTVFPDGTLEVR YAQVQDNGTYL
CIAANAGGND SMPAHLHVRSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNI EIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

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FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAAC
ATCGTAGTCCACCCCCTCCCCATCCCCAGCCCCCGGGATTAGGCTCGCCAGCGCCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGC
TGTTGCGCTGCTGCTGGGCGCCCCGGCGGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGCTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCACAGAAGCCCATCATCACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTCAGTCTTCTGGGAGCAAG
CCTGCAGCCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACCCCAGTCCGGTGCCCT
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTGCTG
CTCATCATGCTCATCTTCTTGGCCACTACTTGATCCGGCACAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTTCATCTAGAGGCGCCTGCCCCACTTCCTGC
GCCCCCAGGGGCCCTGTGGGGACTGCTGGGGCCGTCACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCCCTCCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTTTGTACTCGGTTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTTCCTGCTGCTTCTCTGCATTTGGGTTATTATTATTTTTGTAAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA
AACAAAAACA

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FIGURE 32

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVCLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSSISINVALADEGEYTCSTFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCTTTTCTTCTCCTTTCCTGG
CTTCGGACATTGGAGCACTAAATGAACCTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT
GCTGGAGACGTCTCTTTGTTTTGCCGCTGGAAACGTTACAGGGGACGTTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA
AGTCTGCAGCGTTTCACTGCCCCGACTTCCCAGTTTTTACCATTTATTTCTGCATGGCAATTC
CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGACATGG
AAAACAATGGCTTGCATGAAATCGTTCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTTAAATTTATTACGAGATATAGACCCGGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTTACCTGCCAAC
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCCAAGAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGTCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGGCGCCCCCTG
CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCTTAGCTAACA
GTTTACCCTGCCCTGGGGGCTGCAGCTGCGACCACATCCCAGGGTCCGGGTTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCAGGA
GCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACACTTTCAAG
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA
GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCCGGGCACTTTCAATGCCATGCCCAAACCTGAGGATCCTCATTCTCAACAACAACCTG
CTGAGGTCCCTGCCTGTGGACGTGTTTCGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCACAA
CAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCA
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTTCTT
TAGAAAGGATTTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTTGGCGGAGACCGGGACGCACTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCGGGACTGCTGCTGGT
GTTTGTACCTCCGCCTTCACCGTGGTGGGCATGCTCGTGTTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCCTACAGACAGTCTGT
GACTCTTCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTAAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCG
ATACATCCTTCCCCACCGCAGGCACCCCGGGGGCTGGAGGGGCGTGTAACCAATCCCCGCG
CCATCAGCCTGGATGGGCATAAGTAGATAAAATAACTGTGAGCTCGCACAACCGAAAGGGCCT
GACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
GCCAGCTCGCTCTTTGCTGAGAGCCCCCTTTTGACAGAAAGCCCAGCACGACCCTGCTGGAAG
AACTGACAGTGCCCTCGCCCTCGGCCCGGGGCTGTGGGGTTGGATGCCGCGGTTCTATAC
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTTTCCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT
TGTAATAAGTAACTTTGACTTCTGAC

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FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNKKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAQDLNKLVLILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPEYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANSRPCPGGCSCDHIPGSGLKMNCCNNRNVSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLDDLRLWLYMDSNY
LDTLSREKFAGLQNLLEYLNVEYNAIQILIPGTFNAMPKLRLILNNNLLRSLPVDVFAGVSL
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGPNWECSTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLLVFVTSFTTVVGMVLFILNRNRKRSKRDRANDSSASEINSLQTVCDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

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FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCTTGACCCAGAAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTGCGGGCCTAAGGGAAACTGTTGGC
CGCTGGGCCCCGCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGG
AAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCGGGGCCTCAG
AGAATGAGGCCGGCGTTTCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCGGGCGG
CGGCGAACACCCCACTGCCGACCGTGCTGGCTGCTCGGCCTCGGGGGCCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGCGTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCCAGG
GCCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCCACT
GCACCCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCCTCCGACCCCGGCGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGC
GGTACTCCAGGCCACCGGTGGGGTTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCTGCGCCGCGCCCCGGG
GCCGCCTCTAACTTGAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGGACAGCTCCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTGCCCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG
CTTTGCCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCA
GTGGGGAAGGACAGCCGACCCTTGGGGGGACCGGGGTGCCACCAGGCGCCCGCGGCCACT
GCAACCAGCCCCGTGCCGAGAGAAATGGCCAATCAGGGTCGACGAGAAGCTGGGAGAGAC
ACCACTTGTCCCTGAACAAGACAATTCAGTAACATCTATTCTGAGATTCTCGATGGGGAT
CACAGAGCACGATGTCTACCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCTCTGCCACTCCTCAGGCTTT
CGACTCCTCCTCTGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCT
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTCACGAAAGCCCCCTCTTCCCAGCCA
AGGAAGGAGTCTATGGGCCCCGCGGGCCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCCCTTGTGGCGGAGTCCCCTCTTGGCTCTAGTGATGCATAGGGAAACAGGGGA
CATGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACTTAC
TTGTGTAACCTGACAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCCTTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCCTTTAGGA
TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTCGGAGAA
TTTGGAGAAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATATAATTTACA
TTAAAAAATAATTTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTTCAAGGCTAGGAGTAT
ATTGGTTCGAAATCCCAGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

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FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAEEACILRGGALS
TVRAGAE LRAVLALLRAGPGPGGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRCVTS GEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPPIRVDEKLGETPLVPEQDNSVTISIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTM TVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

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T08170 02360660

FIGURE 37

CGGACGCGTGGGATTTCAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCTCCGCCCTGCCGGCCGCGTATC
CCCCGGCTACCTGGGCGCGCCCGCGGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGTGCCGGCGCGCGCGCCGTGGGGTGCAAACCCGAGCGTCTACGCTGCCATGA
GGGGCGCGAACGCCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTTCTGGAGTGTACCTTCAAATAGCAAATGTACTTGGAATCA
CAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTCATAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTGGCCG
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAAC
CCCCAACTGGCCAGACCGGGATTACCCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTTAAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGAAA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACTTCTTATTCAGT
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTTATTGGTCACTACATATTCAGGCCAAAA
AACTGCCTACAACACAGAACAGCCTGTCACCACCACATTCCCTGTAACCACGGGTTTTAAA
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACACCATCACTCGCGATGGGAGTTTG
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTACAGCAGGCGGG
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG
TTAAACAGTGAAGTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTT
TCTCAGTAGAAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTT
TGCCTGCTGTCAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAGCGTTTATTTATACATCTCTGTAAAAGGAT
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATATTTATAGT
GTTATTTGTTTACCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGCGTTTTCTA
AATCAATGCTTAATAAAATATTTTTTAAAGGAAAAAAAAAAAAA

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FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFCTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVLNFRFIDLESDNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSEARNELLI
QFLSDLSLTADGFIGHYIFRPKKLPPTTTEQPVTTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

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FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTG
CCGGGGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCACAAGCAGCAGGAGGCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCTGAAGCTCTGCTGCCCCGCAGGCACCTTCGGGCCCTCCTGC
CTTCCCTGTCTTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT
TTTGGCCCCCTGTGCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAAC
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTGAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCCCAGAGCTTGGGCTGCCC
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTTTGTAGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTTTCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT
TCTGTGTTACACATCCCCACACCCCATTGCCACTTATTTATTCATCTCAGGAAATAAAGA
AAGGTCTTGGAAAGTTAAAAA

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FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCPPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDQAG
YGGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGPESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDLVVLQQMFFG
IIICALATLAAKGLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT
GCCCCACCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGCGCCCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTTGCCTCGCAGGGGGC
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTGGACCTTGGGGACTATGGAG
CTCAGGGCGACTGTGACCCTGAAGCACCATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGGATGAAGTGGGCGGAGAACTGGGTGCTGGAGCCCCCGGGCTT
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCCTTCAAGTGGC
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCAAGGAGGCTCCAGCCATTAGGCGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTTCGAGGGTACCAGGAGAGCTG
GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT
CCTCTGACAAGTTACCTCACCTAATTTTTGCTTCTCAGGAATGAGAATCTTTGGCCACTGGA
GAGCCCTTGCTCAGTTTTCTCTATTCTTATTATTCACTGCACTATATTCTAAGCACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCCANTGTGTCATTGTTTACTTGTCTGTAC
TGGATCTGGGCTAAAGTCCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAAACATGAATAAAACACATTTTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFSQSFRVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

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FIGURE 43

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGACAAA
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCCAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCT
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGTGTCGTGGCAGCCGTCCTTGTAACCCTGATTCTCCTGGGAAT
CTTGGTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCCTGGTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCTTACT
CAGGTGCTACCGGACTCTGGCCCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTTCTTACCACTGCTGAGTGGCCTGGAACCTGTTTAAA
GTGTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGGTTCGAGGAATCTGCACTCAACTGCCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG
TGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAAGTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTTCGGGAGTTCGGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

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FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW
KFDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYS RGHFDR TKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

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FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCGCAGGCCCCAGCTCAG
GCTCGTGCCCACCCACCAAGTTCCAGTGCCGCACCAGTGGCTTATGCGTGCCCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCCACCGCCCCCTGGCCTCCCCTGCCCCCTGCACCGGCGTCA
GTGACTGCTCTGGGGGAAGTGAACAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGAC
CTCGCTGCCCTTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAAGTGGCCCTGGAGATTGAGGGTCCC
TGGAACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

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FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKQCR
TSGLCVPLTWRCRDLDCSDGSDEEEECRIEPTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL
RNC SRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTS LRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

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FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG
GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCTAGGCTGGATCCCAAGTGA
TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTCATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTTATTATGTGCGCATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTTCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGTCT
GCCACCCGCGGCCTTGTGAGCGCTACAACCACGGAAGTGTGGTGGAGTTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTTCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCCTCCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGTCTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCTCCCCGGAG
TTCCAGCAGTGACCCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCTTAGGCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCCCTTACCCGTGGACGACCAGAGCCCCCAGCATAACCCGGCTCAGGGGACACGGA
CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA
GTCTGTATTACCTCCCAGGTGCCAAGAGAGCACCCACCCTGCTTCGGACAACCCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATCATGCCCACTGGGT
GTTGTTCTTAAGAACTGATTGATTAAAAAATTTCCCAAAGTGCTCCTGAAGTGTCTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCCTTTCTTCTTGGTTTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC
CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAGNAAAAA

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FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLLVLLLVLARMFQTKFKAHFPPRGPPRSSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

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FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCGGTGGCCTAGAGA
TGCTGCTGCCGCGGTTGCAGTTGTCGCGCACGCCTCTGCCCCGCCAGCCCGCTCCACCGCCGT
AGCGCCCCGAGTGTCTGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTTA
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAA
AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGACTGATGGCAGCATAT
CACAATTTAGGAACTGGTATGTGGATGAGCCGTCCTGCGGCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGA
CCGGTGCAACATGAAGAACAATTTCAATTTGCAAATATTCTGATGAGAAACCAGCAGTTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT
CCTAATCCCCAGCATTCCCCTTCTCCTCCTCCTTGTGGTCACCACAGTTGTATGTTGGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC
TGGCCCTCTCCTCACCAGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTT
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTTGTGACCAATGACATTTATGA
GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC
CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCCAGGTCTGGCACATAGTA
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG
GCAGTGATAAAGATGGGCTGTGGAGCTTGGAACACCTCTGTTTTCTTGCTCTATACAG
CAGCACATATTATCATAACAGACAGAAAATCCAGAATCTTTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAAAAA

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FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSI ESEDEQKLI EKFIENLLPSDGD F WIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAA NLAYILIPSIPLLLLLLV
VTTVVCWVWICRKRKREQPD PSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTTGCCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAATC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT
GCAGCAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTTCGTTCCACTAACATTTTTTCGGAATCTG
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTCAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTGAGAAGTCTTGATCCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTTGACCACAAATGGCCACCGTTTGCT
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTTATACCTTAAGCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCTTTATACAATG

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FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMOVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQOMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTGRRRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

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FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCAATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCTAGCGTCTCCATCTGGAGTGC GGCTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA
GTCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTTCA
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACCTGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTCTGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCCTGATTCTCAGGCCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACCTACATCA
CCACCTTTCCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCATTTGTCCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAGGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTTATTTACAATAATAAAGATAGCAC
TATGTGTTCAAA

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F08T40-02E6660

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVTCQTGWSLRAAKVVCRLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGWVGSVCCDNWGEKEDQVVKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

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FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTCCGGCTGCCTGGG
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
TGTGGACAAGAGGGTCATGGAGACAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTGCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTTGTCTCACAAGTGGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACT
AAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL
VNNAGISYRGTIMDTTVDVVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

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FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTTAA
GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTTATACCTTTGT
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA
GGCATTCTTCTCCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA
TTTCATAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
TCTGTGTCTTAATTTTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCCTGAGCGTTT
CCTGGCAGTTTTAAACGAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAAGCACCTAGTTTTCTGAAAACCTGATTTACCAGGTTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTTTAATGTTTGAACCTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA
TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA
CCAAAATGACTTTATTAAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
AATTTGTACCATAACCGTTTATTTAACATATATTTTTATTTTTGATTGCACTTAAATTTTGT
ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTTACAATGAATATCATGAACTCTCAATGGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AA
AAA

FIGURE 58

MKFLLDIILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

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FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTGCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGGCTC
AGGGAGGAGCACC GACTGCGCCGCACCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCCTGTTGATGCCTGGCCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
GTTTCCATGCCACCTAAGGGGAGACTCAGGACAGCCATTATTTCTCACCCTTACATTGAAGC
TGGGAAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCTCACCCTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTC
TTCCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG
AGGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCCTTATGTTGTCACAAGTAACATGA
CCTTGCGTGACAGAGACTTCCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
AGCACGGGATTTATACAGTGCACCTAATTGAGTTTTTCCAGATATTTCTGAATATAAAAAATA
ATGACTTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTTGGAGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGT
GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTTGTCACTCCCAGAGGTGAGACAA
GCCATCCACGTGGGGAATCAGACTTTTAATGATGGAATATAGTTGAAAAGTACTTGCGAGA
AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTTGGAAGATCTTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGAATCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA
TTCATTTATGGAAAAGGATGGGATCCTTATGTTGGATAAACTACCTTCCCAAAGAGAACAT
CAGAGGTTTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTTCATATCTGCAAGATTTTTTTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGC
TTTTGTTTTTGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
AATTTTAGGGTCTTGAATAGGAAGTTTTTAATTTCTTCTAAGAGTAAGTGAAAAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCCAAATAAATGGATGAAGCTATAA
TAGTTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAATA
AAAATATTATATATAAAAGTAAAAAAA

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FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGD SGQPLFLTPYIEAGKIQKGRELSL
VGPFPGGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVT SNMTLRDRDFPWT T T L S M L Y I D N P V G T G F S F T D D T H G Y A V N E D D V A R D L Y S A L I Q F
FQIFPEYKNND FYVTGESYAGKYVPAIAH LIHSLNPVREV KINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNV TG
CSNYYNFLRCTEPEDQLYYVKFSLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVL IYNGQLDIIVAAAL TERSLMGMDWKGSQEYKKA EKKVWKIFKSDSEVAGYIRO
AGDFHQV IIRGGGHILPYDQPLRAFD MINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

09009320-01801
FOOTNOTES

FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACAT
TTTTCCCTTTCTAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGCCTGCCTAACAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCTAATATCAAATTGACTGGCTGGG
TGAACCTCAACAGCCTTTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTTGTAAAATAAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAAGAGGGAGAAAGTATGTTAAAAATA
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCCTGGGTC
AGGCCAGCCTCTTTGCTCCTCCCGGAAATTATTTTGGTCTGACCACTCTGCCTTGTGTTTT
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGTCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCCCCAGCAGCCGGC
ATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT
CCACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTCATAAGACAGGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCCCTCATCGTGAGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGTCTGCA
AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCCA
GCCGGAAGCTGCCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACAT
CTTCTACATCTACGGCTTTGCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGCGG
CTCTGCAAGGATGACCCCAAGTTCCACTCATACTGTCCCTGCCCTTCGGCTGCACCCGGGC
CGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC
AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCAAAGGGCAGAAG
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGGAAGGACGTCCAGTGACGAAGGCGCCTGTCCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACCAGCCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC
ATTACCTCCTCAGCAAAGAGTCCCTCTTGAAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTTATTTTCTTGGGGAACAAAGGTGAATGGGGAGGTAAGAAGGGGTAAATTTTGTG
ACTTAGCTTCTAGCTACTTCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
TTTCAATATTTCCCAAACCTTTAAGAAAAAATTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSHDHSAFCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPPEEDNKSRYPLIVQPCSEVLTLTNVNKLLIIDYSENRLLAGSL
YQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPRDPRESSAMLDYELHSDVSSLIKIPSDTLALVSHFDIFYIYGFASSGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSAFCAPPIRAINLQIKERLQSCYQGEGN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTGSGKLKKVRVYEFRCSSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

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T08T20 02E60660

FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGCGGACTGGAGTGGGAACCCGGGTCCCGCGCTTAGAGAACACGCGATGACCA
CGTGGAGCCTCCGGCGGAGGCCGCGCCCGCACGCTGGGACTCCTGCTGCTGGTCTTGGGCTTCTGGTGCTCC
GCAGGCTGGACTGGAGCACCTTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTTCGGGGGCTCCATCCACTATTTCCGTGTGCCAGGGAGTACT
GGAGGGACCGCCTGCTGAAGATGAAGCCTGTGGCTTGAACACCCTCACCACCTATGTTCCGTGGAACCTGCATG
AGCCAGAAAGAGGCAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCTTCGTCTGATGGCCGAGAGATCG
GGCTGTGGGTGATTCTGCGTCCAGGCCCCCTACATCTGCAGTGAGATGGACCTCGGGGGCTTGCCAGCTGGCTAC
TCCAAGACCCTGGCATGAGGCTGAGGACAACCTTACAAGGGCTTCACCGAAGCAGTGGACCTTTATTTTGACCACC
TGATGTCCAGGGTGGTGCCACTCCAGTACAAGCGTGGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATG
GTTCCCTATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCAGTGGAGGACCGTGGCAATTGTGGAACCTGC
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTCTTGGCCACCATCAACTTGCAGT
CAACACACGAGCTGCAGCTACTGACCACCTTTCTCTTCAACGTCCAGGGGACTCAGCCCAAGATGGTGATGCGAGT
ACTGGACGGGGTGGTTTGACTCGTGGGGAGGCCCTCACAATATCTTGGATTCTTCTGAGGTTTGTGAAAACCGTGT
CTGCCATTGTGGACGCCGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATG
GAGCCATGCACCTTCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG
ATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG
ACCTTCTTCCCAAGATGCGGTATGAGCCCTTAACGCCAGTCTTGACCTGTCTCTGTGGGACGCCCTCAAGTACC
TGGGGGAGCCAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCCCT
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG
TGTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT
ACACCGTGCTGAGGATCTTGGTGGAGAATCGTGGGCGAGTCAACTATGGGGAGAATATTGATGACCAGCGCAAAG
GCTTAATTGGAATCTCTATCTGAATGATTCAACCTTGAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTTCAGAGGTTTCGGCCTGGACAAATGGNGTTCCCTCCCAGAAACACCCACATTACCTGCTTCTTCTTGG
GTAGCTTGTCCATCAGCTCCACGCCTTGTGACACCTTTCTGAAGCTGGAGGGCTGGGAGAAGGGGTTGTATTCA
TCAATGGCCAGAACCTTGGACGTTACTGGAACATTTGGACCCAGAGAAGACGCTTTACCTCCCAGGTCCCTGTTGA
GCAGCGGAATCAACCAGGTATCGTTTTTGGAGGACGATGGCGGGCCCTGCATTACAGTTACCGGAAACCCCCC
ACCTGGGCAGGAACCAGTACATTAAGTGAAGCGGTGGCACCCCTCCTGCTGGTGCCAGTGGGAGACTGCCGCCTC
CTCTTGACCTGAAGCCTGGTGGCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGG
ACTGGGGGCTACAGTCTGCCCCGTCTCAGCTCAAAACCTAAGCCTGCAGGGAAGGTGGGATGGCTCTGGGGCC
TGGCTTTGTTGATGATGGCTTTCTACAGCCCTGCTCTTGTGCCGAGGCTGTGCGGCTGTCTAGGGTGGGAGC
AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGCTGAAACGTGCCCTTGACCCGGACGTCACAGCCC
TGCGAGCATCTGCTGGACTCAGGCGTGCTCTTTGCTGGTTCCTGGGAGGCTTGGCCACATCCCTCATGGCCCCAT
TTTATCCCCGAAATCCTGGGTGTGTACCAAGTGTAGAGGGTGGGGAAGGGGTGTCTACCTGAGCTGACTTTGTT
CTTCTTCAACCTTCTGAGCCTTCTTTGGGATTCTGGAAGGAACTCGGCGTGAGAAACATGTGACTTCCCCTT
TCCCTTCCCCTCGCTGCTTCCACAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCCTCACCCTGCGTCTTCC
CAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCA
CATCCAGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCC
AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGA
GGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGG
ACAGAAGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCACGCCCCAAGCAGGAGGAGGAGGAGGAGGAGGAGG
GAAGTGTGTCCAAGTCCGCATTTGAGCCTTGTCTGGGGCCAGCCCAACACCTGGCTTGGGCTCACTGTCTGA
GTTGCAGTAAAGCTATAACCTTGAATCAAA

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FIGURE 64

MTTWSLRRRPARTLGLLLLLVVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW
IFGGSIHVFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDFSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVDLYFDHLMSRVVPLQ
YKRGGPPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKDGLSKGIVQGVLAT
INLQSTHELQLLTFFLFNVQGTQPKMVMHEYWTGWFDWSGGPHNILDSSSEVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYILYE
TSITSSGILSGHVHDRGQVFVNTVSIQFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSPKKNFRIYSLDMKKSFFQRFGLDKWXSLETPETPLPAFFLGSLISIS
STPCDTFLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
CTGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGGCTCGGCCCCGAGGCCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
AAGAAGCTGTCTTGCCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCA
GGCAGACACTCGGTTCGTTCTAGTGGATAGGGGTTCATGACCGGTTTCTCCTAGACGGGGCCC
CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCCGAC
CGGCTTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTTATGTGCCCTGGAACCTA
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCCTC
AGATCCAGACTTCCTTGCCGCAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATC
CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTACAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGGCTCTTCCGTGCACTGCTAGG
AGAAAAGATCTTGCTCTTCACCACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GACTCTATACCACTGTAGATTTTGGCCCAGCTGACAACATGACCAAAATCTTTACCTTGCTT
CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGGCCAGAATCACTCCACACGGTCTGTGTCTGAGTGTAAACCAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTTGCTCTTCGAGATGTCATCAGCAAGT
TCCAGGAAGTTCTTTGGGACCTTTACCTCCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCCAT
TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC
GAACCTATATGACCCATAACATTTTGGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTC
CATGACCGTGCTATGTGATGGTGGATGGGGTGTTCCAGGGTGTTGTGGAGCGAAATATGAG
AGACAAACTATTTTTGACGGGGAAACTGGGGTCCAACTGGATATCTTGGTGGAGAACATGG
GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG
GGGCAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
GTGGTTTTCCCCTCCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT
ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACTTGGGCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCTCTACGTGCCAAGATTCTGCTGTTTCTAGGGGAGCCCTCAACAAAATTA
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTTGGATAAGCCTATC
CTCAATAGCACTAGTACTTTGCACAGGACACATATCAATTCCCTTTCAGCTGATACTAGG
TGCCTCTGAACCAATGGAGTTAAGTGGGCACTGAAAGGTAGGCCGGGCATGGTGGCTCATGC
CTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAGGACTTCAAGA
CCAGCCTGGCCAACATGGTGAACCCCGTCTCCACTAAAAATACAAAAATTAGCCGGGCGTG
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAAAA

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FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDGRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVD FGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWKQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

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FIGURE 67

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTCAGGATACCTTTGAAGGAATATT
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT
GCGTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT
CTTGTCAGAAGTTAGTGAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG
AAAACTCAGGCAGCACATTTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTTCATG
CTGTCGGGGGTGCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTTCTCCACGTGAAGAGCAATTTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTACATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACTGGAT
TTAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAACGACT
GACTTGTTTTAAATTTATGGCATAACAAAATTGTTACTATTCTCCCTCTATTACCCATGTCA
AAAACCTTGGAGTCACTTTATTTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAACTG
CTTGACCGCCTGCCAGCCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAGCGGGCTTGTTG
TGGAAGATCACCTTTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTTGCAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
ATACATCTTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTTGTAGGGTTTTAAGTCATTCATTTCCAAATCATTTTTTTTTTTCTTTTGGGG
AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTTCTTTTTTAAATTGTTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAA

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FIGURE 68

MAYMLKKLLISYISIIICVYGFICLYTLFWLFRIP LKEYSFEKVREESSFSDIPDVKNDF AFL
LHMVDQYDQLYSKRFGVFLSEVSENKLR EISLNHEWTFEKL RQHISRNAQDKQELHLFMLS G
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLES LREL RHLKILHVKS NLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNC ELERIPHAIFSLSNLQELDLKS
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLES LYFSNNKLES LPPVAVFSLO
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDH LFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCCATTCTTTTCATTGACAACTGACTTTTTTTATTTCT
TTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATAAGGAT
CTGTGTTTTGGGGTTTTCTTCTCTCCCTGACATTGGCATTGCTTAGTGTTGTGTGGGGAGGGAGACCACGTGG
GCTCAGTGCTTGCTTGCACTTATCTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTC
ATCGCTGGTGGTATCCTGGCGGCCTTGCTCCTGCTGATAGTTGTCGTGCTCTGTCTTTACTTCAAATACACAAC
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAACCCAGACAAGGTGTGGTGGGCCAAG
AACAGCCAGGCCAAAACCATTGCCACGAGTCTTGTCTGCTGCCCTGCAGTGCTGTGAAGGATATAGAATGTGTGCC
AGTTTTGATTCCCTGCCACCTTGCTGTTGCGACATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAA
GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAG
CTCCCCATCAGTTTTCATGGAAAATAACTCAGTGCTGCTGGGAACCAAGCTGCTGGAGATCCCCTACAGAGAGCTTC
CACTGGGGGCAACCCCTTCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGGAATGCTGATAAACCAAGTCA
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCTGGAACCTGACGTTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCCTATAAAAGCTGTGCGTCTTAAGGCTGCCAGCGCCTTGCCAAAATGGAGCTTGTA
AGAAGGCTCATGCCATTGACCCTCTTAATTCTCTCCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAGACCAGAAAACAAAAGCATCAGAATTATCTTTCTATGTCCAGCTT
GATCCAGATGGAAGCTGTGAAAGTGAAAAACATTAAGTCTTTGACGGAACCTCCAGCAATGGGCCTCTGCTAGGG
CAAGTCTGCAGTAAAAACGACTATGTTCTGTATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCTAACATCTCTATTCCAACTGT
GGCGGTACCTGGATACCTTGAAGGATCCTTCACCAGCCCCAATTACCCAAAGCCGCATCCTGAGCTGGCTTAT
TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAACTAAACTTCAAAGAGATTTTCCCTAGAAATAGAC
AAACAGTGCAAAATTTGATTTTCTTGCCATCTATGATGGCCCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGT
GGCCGTGTGACTCCACCTTCGAATCGTCATCAAACCTCTGACTGTCTGTTGTCTACAGATTATGCCAATTCT
TACCGGGGATTTTCTGCTTCTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAATAACTTGCAACTAAAA
GACCCAACTTGCAAGACCAAATATCAAATGTTGTGGAATTTTCTGTCCCTCTTAATGGATGTGGTACAATCAGA
AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACC
CGTCAGAAAACAACTCCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA
GAAGATGATGTAATACAAAGTCAAATGCACCTGGGCAATATAACACCAGCATGGCTCTTTTGAATCCAATTCA
TTTGAAAAGACTATACTTGAATCACCATATTATGTGGATTGTAACCAAACTCTTTTGTTCAGTTAGTCTGCAC
ACCTCAGATCCAAATTTGGTGGTGTCTTGTATACCTGTAGAGCCTCTCCACCTCTGACTTTGCATCTCCAACC
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTTTGTAAGGTGTATCCCTTATTTGGACACTATGGGAGA
TTCCAGTTTAATGCCCTTAAATTCTTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAGTTTTGATATGTGAT
AGCAGTGACCACCAGTCTCGCTGCAATCAAGTTGTGTCTCCAGAAGCAAACGAGACATTTCTTCATATAAATGG
AAAACAGATTCCATCATAGGACCCATTTCGTCTGAAAAGGGATCGAAGTGCAAGTGGCAATTCAGGATTTTCAGCAT
GAAACACATGCGGAAGAACTCCAAACCAGCCTTTCAACAGTGTGCATCTGTTTTCTTTCATGGTTCTAGCTCTG
AATGTGGTGACTGTAGCGACAATCACAGTGAGGCATTTTGTAATCAACGGGCAGACTACAAATACCAGAAGCTG
CAGAACTATTAACTAACAGGTCCAACCCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTATGAATAAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGTAAAAAAA

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FIGURE 70

MELVRRRLMPLTLLILSCLAELTMAEAEAGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIFSIVQLDPDGSCENIKVFDGTSSNGPLLQVCSKNDYVPVFESSSSTLT
FQIVTDSARIQRTVFVFFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDFLAIDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTIKLESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDIIIGPIRLKRDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGCTGC
TGCTGCCGCGCCGCGCGCTGCCCTGCCACAGCGCCACGCGCTTCGACCCACCTGGGAGTCC
CTGGACGCCCCGCGAGCTGCCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG
GGGAGTGTTTTCCGTGCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAAGGAAA
AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAATATGAAGAT
TTTGGACCACTATTTACAGCAAAATTTTTTAATGCCAACCAGTGGGCAGATATTTTTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT
CAGAATATTCGTGGAACCTGGAATGCCATAGATGAGGGGGCCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTTTGACTGTACTATTCCCTTTTTTGA
ATGGTTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT
ATATAATGAAAGCCCAGTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA
CATAAATGGGAAAACCTGCATGACAATAGACAACTGTCCTGGGGCTATAGGAGGGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTCATGTG
GAGGAAATCTTTTGATGAATATTGGGGCCACACTAGATGGCACCATTTCGTAGTTTTTTGAG
GAGCGACTGAGGCAAGTGGGGTCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCACATCAGGACAGCTGTTCTTGGCCAT
CCCAAAGCTATTCTGGGGGCAACAGAGGTGAACTACTGGGCCATGGACAGCCACTTAACTG
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTTCATCAGATGC
CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAAACTGGATAAGAAAATTATTTGGCAGTTCAGCCCTTTCCCTTTTTTCCCACTA
AATTTTTCTTAAATTACCCATGTAACCATTTTAACTCTCCAGTGCACCTTGCCATTAAAGTC
TCTTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAAT
TTTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAAATACTGTAAAATAAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAAA
GTTTTTCTTTCTTCAATTATAAATTAACATAAGTGTACTGTAACCTTACAAACGTTTTAATT
TTTAAAACCTTTTTTGGCTCTTTTGTAAATAACACTTAGCTTAAAACATAAACTCATTGTGCAA
ATGTAA

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FIGURE 72

MRPQELPRLAFPLLLLLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYWQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKKGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

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FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT
TTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCCTTGTGAGCAAAAAGGCGAACCAGC
AGCTGAATTTACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGGAGA
TGGATTTCGTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
TCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGAT
ACTTGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCA
AACTGCAACACAAACAACAGAATTTATTGTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTT
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAATTGATTTGTGTACACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAAAC
TGAACCATTTGTTGAAAAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGC
TATGTCAAAGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGA
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAA
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTTCTTTCATGCTCC
TTACCCCTGCCCCAGCTGGGGAAATCAAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCCTT
GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC
CCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCC
TTTCTAGCCTGGCTATGTCCTAATAATATCCCCTGAGGAGAAAGGAGTTTTTGCAAAGTGCAA
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGG
TGGGTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGAC
CCTTCTTTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTTCTGAGCCCGGTA
AGAGCAAAAGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGA
ATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT
AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCA
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATATTTCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTCA
GTTTTGATATTTCTAGCTTATCTACTTCCAACTAATTTTTTATTTTTGCTGAGACTAATCTT
ATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAACATACCTAAGAAG
TACATTGTTACCTCTATATACCAAAGCACATTTTAAAAAGTGCCATTAAACAAATGTATCACTA
GCCCTCCTTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAA
AGCATTTAGAAACTT

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FIGURE 74

MARCFSLVLLLLTSIWTTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLWKPVSROF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFFFTNKNQOKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

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FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGATTTCGGTGCCGCGACTTTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTGCGCCCTGCTCTCTGCTGCCTTCCTACTCGTGAGGAA
ACTGCCGCGCTCTGCCACGGTCTGCCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT
TCTTTTCTTCCGCTTGGATATTCGCATGGGCCTACTTTACATCACACTCTGCATAGTGTTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAA
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAAC
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGA
TGGGGAAAACAAGAAGGATAAATAAGATCCTCACTTTGGCAGTGCTTCCTCTCCTGTCAATT
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGG
CTGNGACTGGNTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG
GCACCCTACAGGAAGGCCTGCCATGCTGTGGCCAACCTGTTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGGAAATGGTTTCCCTCCAAGCTTGGGTCACTGTGTTAACTGCTTATC
AGCTATTCAGACATCTCCATGGTTTCTCCATGAAACTCTGTGGTTTCATCATTCCTTCTTAG
TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAA
CGCTAAGAATTTTCCCCCAAGGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTC
TTCATTAAAAGTATAAGCCTAACTTTGTCGCTAGTCCTAAGGAGAAACCTTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGAGAGAGAAATCCCCTGGACTTTCAC
TAACCCTCTGACATACTCCCCACACCCAGTTGATGGCTTTCGTAATAAAAAGATTGGGATT
TCCTTTTG

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FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVRLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGCGGCCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGGACGTTTGCCCTG
GGGCCCCAGCCTGGCCCCGGGTCAACCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCCA
TTGCTCCTGCTGCCCGGCTCCTACGGACTGCCCTTCTACAACGGCTTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCTGTTACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGGCGTGTGCGTGTCAAATGGTGGAAAGCT
GTCGGAGAACGGGGCCCCAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCT
TTGGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGGCTGGAGGACTATGGGCGTTACCGCTGTGAGGTCATTGACGGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGTCTTTCCTTACCAGTCCCCCA
ACGGGCGCTACCAGTTCAACTTCCACGAGGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGTG
GTGGCCTCCTTTGAGCAGCTCTTCCGGGCCTGGGAGGAGGGCCTGGACTGGTGC AACGCGGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCCGGCAGCCCTGCGGTGGCC
CAGGCCTGGCACCTGGCGTGC GAAGCTACGGCCCCCGCCACCGCCGCCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGGCGGGTGTACTACCTGGAGCACCTGAGAAGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATCGCCAAGGTGGGAC
AGCTCTTTGCCGCTGGAAGTTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCTGTGGTTCACCCGCATCCTAACTGTGGGCCCCCAGAGCCTGGGGT
CCGAAGCTTTGGCTTCCCCGACCCGCAGAGCCGCTTGTACGGTGTTTACTGCTACCGCCAGC
ACTAGGACCTGGGGCCCTCCCCTGCCGCATTCCCTCACTGGCTGTGTATTTATTGAGTGGTT
CGTTTTCCCTTGTGGGTTGGAGCCATTTTAACTGTTTTTATACTTCTCAATTTAAATTTTCT
TTAAACATTTTTTTTACTATTTTTTTGTAAAGCAAACAGAACCCAATGCCTCCCTTTGCTCCTG
GATGCCCCACTCCAGGAATCATGCTTGCTCCCCTGGGCCATTTGCGGTTTTGTGGGCTTCTG
GAGGGTTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCCAGAGTGGGC
GGTGGCCTGTCTAGAATGCCGCCGGGAGTCCGGGCATGGTGGGCACAGTTCTCCCTGCCCT
CAGCCTGGGGGAAGAAGAGGGCCTCGGGGGCCTCCGGAGCTGGGCTTTGGGCCTCTCCTGCC
CACCTCTACTTCTCTGTGAAGCCGCTGACCCAGTCTGCCCACTGAGGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGGAAGGAAGAACTCCCCCTCCCCGTTCCCT
TCCCCTCTCGGTTCCAAAGAATCTGTTTTGTGTGTCATTTGTTTTCTCCTGTTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTGTACTTTGGACAATAAATGGTGTCTATGACTGCCTTCCGCCAA
AAA
AAA

FIGURE 78

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRLLHRYDVFCFATALKGRVYYLEHPEKLTLTAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGCGGGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAA
CTTCCAGTACGACCATGAGGCTTTCCTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCA
CCCCAGAGGAAAGCCAGGCCCGTCTGGGGCGGATCGTGACCGCATGGACCGCGCGGGGGAC
GGCGACGGCTGGGTGTCGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCA
CATACGGGACTCGGTGAGCGCGGCCTGGGACACGTACGACACGGACCGCGACGGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCCGGTGAAGAATTTTCATGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGGCGTTTCCGGGTGGC
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGG
AGTTCCCTCACATGCGGGACATCGTGATTGCTGAAACCCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTTCCGGGACTTCCGGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCCAGGACCAGCCC
CTGGTGGAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAA
AGCGGAAATCCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGGCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCGCAGGAG
GCAGATGCAGTCCCAGGCATCCTCCTGCCCCCTGGGCTCTCAGGGACCCCTGGGTCTGGCTTC
TGTCCCTGTACACCCCCAACCCAGGGAGGGGCTGTATAGTCCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCTTGGCCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCCT
GGCCCCAGCCCTCTCCTGCCTGGCCTGGCCTGGGACACCTCCTCTCTGCCAGGAGGCAATAA
AAGCCAGCGCCGGGACCTTGAAA
AAAAAAAAAAAAAAAAA

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FIGURE 80

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAAWVQTERQQ
FRDFRDLNKDGHLDGSEVGHVLPAPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCGGGCGCGGGTGCGAGGGATCCCTGACGCCCTCTGTCCCTGTTTCTTTGTGCTCCAG
CCTGTCTGTCTGTCGTTTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTTCACACCGATCCTG
GGCTTCGCTCGATTTGCCGCCGAGGCGCCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG
CGGGTCGTCTGTGTCTCTCTCTCTGCGCCGCGCCCGGGGATCCGAAGGGTGCGGGGCTCT
GAGGAGGTGACGCGCGGGGCCTCCCGCACCTGGCCTTGCCCGCATTCTCCCTCTCTCCAG
GTGTGAGCAGCCTATCAGTCACCATGTCCGCGAGCCTGGATCCCGGCTCTCGGCCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGGGCCGCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG
TTTTACCAGAGGCTTGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGGCTGCC
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAACTATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT
GGTCTGCTTCTTTACAGTAACTAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAAACACCCGAGAAGAAAACTGG
CAATAAAGATTGTAAAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC
GCCGATTTAATTTACAGAAGAATTTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA
GAAGGACCACATGTGGGCCTTGTTCAAGCCAGTGAACATCCCAAATAGAATTTTACTTGAA
AACTTTACATCAGCCAAAGATGTTTTGTTTGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTCACATTTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTTCTCTTACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAAA
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT
CAGTGAACATTGCCTTTCTAATTGATGGCTCCAGCAGTGTTGGAGATAGCAATTTCCGCCTC
ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAAATCTCGGACATTGGTGCCAAGAT
AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTTCACTGACTATAGCACCA
AAGAGAATGTCCTAGCTGTCATCAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT
GATGCCATTTCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAAGAA
CTTCTAGTAATTGTCACAGATGGGCAGTCCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG
CACATGATGCAGGAATCACTATCTTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTTCTTCACAAGAGAGTTTACAGGATT
AGAACCAATTGTTTCTGATGTCATCAGAGGCATTTGTAGAGATTTCTTAGAATCCCAGCAAT
AATGGTAACATTTTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAAATTGTATT
CTCATAATACTGAAATGCTTTAGCATACTAGAATCAGATACAAAATATTAAGTATGTCAAC
AGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT
ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEFVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAlKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI
FSVGVAWAPLDDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

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FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCAGCCC
GGCGGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCCGCAGCGCAACTCGGTCCAGTCG
GGGCGGCGGCTGCGGGCGCAGAGCGGAGATGCAGCGGCTTGGGGCCACCCTGCTGTGCCTGC
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCGGCCCCGGCTCTCAGCTACCCGCAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGA
GGTTGAGGAAGCTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTAT
CACAATGAGACCAACACAGACACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGGCCAGC
ATGTACTGCCAGTTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAAA
TGGCCACCAGGGGCGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGGCTG
TGCTGTGCCTTCCAGAGAGGCCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGA
GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTTGTGCCAGTGCCCTCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCCGCCGCT
GCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA
ATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTACA
TCTTCTTCCCAGTAAGTTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTCAGC
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAAC
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAG
ACAGCCGTTTGTCTACATGGCTTTGATAAATTGTTTGAGGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTCTGATTGGTTTTGGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAA
CCTGGCAAAAATGCAACAAATGAATTTTCCACGCAGTTCCTTCCATGGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTTACCCTGCATTACATGTGTTTATTTCATCC
AGCAGTGTTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTC
CCTCTCTCAGCACAGCCTGGGGAGGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCAT
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTTCTTGAGGCATGCACATCTGGAATTAAG
GTCAAATAATTCTCACATCCCTCTAAAAGTAACTACTGTTAGGAACAGCAGTGTTCTCAC
AGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGT
TGCATTAGTAACTTTGAAAGGTATATGACTGAGCGTAGCATAACAGTTAACCTGCAGAAACA
GTAAGACAATTATCAACCACGTGGAGAAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTTCATCCAGAGTTCCTTAAAGTTTAAAGTTGCACATGATTGTA
TAAGCATGCTTTCTTTGAGTTTTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGC
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 84

MQRLGATLLCLLLAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMMLCTRDSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

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FIGURE 85

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCCTACCTCACATCTCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAATTTTCAGCCCATCCACTCTCCTTCCCTCCCAAACACACATGTGCATGTACACACACACATACA
CACACATACACCTTCTCTCTTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACAC
TAAAGCCTTAAGGACAGGCCTGGCCATTACCTCTGCAGCTCCTTTGGCTTGTTGAGTCAAAAAACATGGGAGGGG
CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTCAGGAG
TTCGAGACCAGCCTGGCCAACATGGAGAAACCCCCATCTCTACTAAAAATACAAAAATTAGCCAGGAGTGTTGGC
AGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGT
CAGCTGAGTGACCGCTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAAACAAACACGGGAGGA
GGGGTAGATACTGCTTCTCTGCAACCTCCTTAACTCTGCATCCTCTTCTTCCAGGGCTGCCCCTGATGGGGCCTG
GCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGAAGAGTGCACGCCG
GTGTAGAATGACTGCCCTGGGAGGGTGGTTCTTGGGCCCTGGCAGGGTTGCTGACCCCTTACCCTGCAAAACACA
AAGAGCAGGACTCCAGACTCTCCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC
ACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCCGTGGTACCCTGGCATGTTCCCTGCCCCCTCA
GTGTGCCCTGCCAGATCCGGCCCTGGTATACGCCCGCTCGTCTTACC CGAGGCTACCCTGTGGACTGCAATGA
CCTATTCTGACGGCAGTCCCCCGGCACTCCCCGAGGCACACAGACCTGCTCCTGCAGAGCAACAGCATTGT
CCGTGTGGACAGAGTGAGCTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTTCGGA
TGCCCGAGACTGTGATTTCCATGCCCTGCCCCAGCTGCTGAGCCTGCACCTAGAGGAGAACCAGCTGACCCGGCT
GGAGGACCACAGCTTTGCAGGGCTGGCCAGCCTACAGGAACCTATCTCAACCACAACCAGCTCTACCGCATCGC
CCCCAGGGCCTTTTCTGGCCTCAGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAG
CCGCTGGTTTGAAATGCTGCCCAACTTGGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATCCTGGACAT
GAACTTCCGGCCCCCTGGCCAACCTGCGTAGCCTGGTGCTAGCAGGCATGAACCTGCGGGAGATCTCCGACTATGC
CCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTCTATGACAACCAGCTGGCCCGGGTGCCAGGCGGGCACT
GGAACAGGTGCCCGGGCTCAAGTTCTAGACCTCAACAAGAACCCTGCTCCAGCGGGTAGGGCCGGGGGACTTTGC
CAACATGCTGCACCTTAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGCCCTGGT
GAACCTCCCCGAGCTGACCAAGCTGGACATCACCAATAACCCACGGCTGTCTTCTATCCACCCCCGCGCTTCCA
CCACCTGCCCCAGATGGAGACCCTCATGCTCAACAACAACGCTCTCAGTGCCTTGACACCAGCAGACGGTGGAGTC
CCTGCCCAACCTGCAGGAGGTAGGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTCTATCCGCTGGGCCAATGC
CACGGGCACCCGTGTCCGCTTCATCGAGCCGCAATCCACCTGTGTGCGGAGCCTCCGGACCTCCAGCGCTCC
GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGGCCCTCATCTCCCCACGAAGCTTCCCCCAAG
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGCTGCATTGCCGGGCACTGGCCGAACCCGAACCCGAGATCTACTG
GGTCACTCCAGCTGGGCTTCGACTGACACCTGCCCATGCAGGCAGGAGGTACCGGGTGTACCCGAGGGGACCCT
GGAGCTGCGGAGGGTGACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGCCAGAACCTGGTGGGGGCTGACAC
TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGGACGAAGGACAGGGGCTGGAGCTCCG
GGTGACGAGAGCCACCCCTATCACATCCTGCTATCTTGGGTACCCCAACCAACACAGTGTCCACCAACCTCAC
CTGGTCCAGTGCCCTCCTCCCTCCGGGGCCAGGGGGCCACAGCTCTGGCCCGCTGCCTCGGGGAACCCACAGCTA
CAACATTACCCGCTCCTTCCAGGCCACGGAGTACTGGGCTGCCTGCAAGTGGCCTTTGCTGATGCCACACCCCA
GTTGGCTTGTGTATGGGCCAGGACCAAGAGGCCACTTCTTGCCACAGAGCCTTAGGGGATCGTCTTGGGCTCAT
TGCCATCCTGGCTCTCGCTGTCTTCTCCTGGCAGCTGGGCTAGCGGCCACCTTGGCACAGGCCAACCCAGGAA
GGGTGTGGGTGGGAGGCGGCTCTCCCTCCAGCCTGGGCTTTCTGGGGCTGGAGTGCCCCCTTCTGTCCGGGTGT
GTCTGCTCCCCCTCGTCTCCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGGAGACACTGTTGCC
ACCATTGTCTCAAAATTTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTACCAAA
AGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGGACCCACGTGCTTGAAGCCTGGCAGCTGGGC
CAAGACAGATGGGGCTTTGTGGCCCTGGGGGTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTCA
CCTCTGCTGCCATTCTGAGGAACATCTCCAAGGAACAGGAGGACTTTGGCTAGAGCCTCCTGCCTCCCCATCTT
CTCTCTGCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCCCTACCTGTGTCCCCGGGCTGCACCCCTTCTCTTC
TCTTTCTCTGTACAGTCTCAGTTGCTTGCTCTTGTGCCCTCCTGGGCAAGGGCTGAAGGAGGCCACTCCATCTCAC
CTCGGGGGGCTGCCCTCAATGTGGGAGTGACCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAA
CGCCTCATCTCAGCAGCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTTGTGGAGAA
ATGTGTACCTCCCCAACCCGATTCACTCTTTTCTCCTGTTTGTAAAAATAAAAAATAAATAAATAAATAA
AAAA

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FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLQLQNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIKDFALVNLP
ELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPPFREMTHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEEAGLYT
CVAQNLVGADTKTVSVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLLAAGLAHLGTGQPRKGVGGRRPLPPAWAFWGSAPSVRV
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT
CTACATGCGGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTCGACGTGGACTGCACCGTGGACATTTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCACCC
CCTGGCCACACTCTTCAAGATCCTGGCGTCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA
GCGCTTCGCCGTCTTCTGTGCGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCGCC
CAGCATTGCCAGCTCACGGGCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAGCGCTGCGCT
GGCCTTCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCGCTGTGGATCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAACCGCTACATCGTCATCGA
CGGGCTGCGGGAGCTCAAACGCCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCAC
AGATGTGGGCGTGCACCTGCAGAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCT
GCACCGCTCACCTGCCTTAAGCTGTGGTACAACCACATCGCCTACATCCCATCCAGATCGGCAACCTCACCAA
CCTGGAGCGCCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCGCGAAGCTGCG
CTACCTGGACCTCAGCCACAACAACCTGACCTTCTCCCTGCGGACATCGGCCTCCTGCAGAACCTCCAGAACCT
AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGAGCTCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCT
GGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGG
CAACCGGCTGGAGTGCTGCTGTGGAGCTGGGCGAGTGCCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCCTGAGCGAG
GCCGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCGGAGGGGCAGGCCCTAGCTTCTCCGAG
AACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCGAGGCTGGGGCCGCTTGTGAGTCAGGCCAGCGGAGA
GGACAGTATCTGTGGGGCTGGCCCCCTTTTCTCCCTCTGAGACTCACGTCCCCCAGGGCAAGTGCTTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTCTGCCCCAGGGGCTGAG
CTGCCACCAGAGGTCTTGGGACCTCACTTTAGTTCTTGGTATTTATTTTTCTCCATCTCCACCTCCTTCATCC
AGATAACTTATACATTTCCCAAGAAAGTTAGCCAGATGGAAGGTGTTTCAAGGAAAGGTGGGCTGCCTTTTCCCC
TTGTCTTATTTAGCGATGCCGCCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCGAACCAG
CCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCCCTCCAGCTGGA
AAGGCCAGGCCCTGGAGCTTGCTCTTCAGTTTTTGTGGCAGTTTTAGTTTTTTTGTTTTTTTTTTTTAAATCAA
AAACAATTTTTTTTAAAAAAGCTTTGAAAATGGATGGTTTGGGTATTAAGAAAGAAAAAAGAACTTAAAAA
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAAAGCAGCCAGACGT
TGAACGTGTGTTTCTTTCCCTGGGCGCAGGGTGCCAGGTGCTTCCGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTTGTTCTTGGGAGGGAGGTTTTTTTTGTTTTTTTTTGGGTTTTTTTTGGTGTCTTGTCTTTCTTCTCTCC
ATGTGTCTTGGCAGGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTTGGCTAATCCCGGATGAACGGTGCTCCATTGCGACCTCCCCTCCTCGTGCCTGCCCTGCCTCTCCA
CGCACAGTGTTAAGGAGCCAAGAGGAGCCAATTGCCCCAGACTTTGTTTTCCCCACCTCCTGCGGCATGGGTGTGT
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTGCGCACCTGGTCTTTCATGAAGAGCAGACACTTA
GAGGCTGGTCCGGGAATGGGGAGGTGCGCCCTGGGAGGCGAGGCGTTGGTTCCAAGCCGGTTCCCGTCCCTGGCGC
CTGGAGTGACACAGCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTT
AGAAGGGTCCCCGCTTAGATCAATCACGTGGACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATGT
CCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCGTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAATAAA
ATCTATAACAGAAAAA

FIGURE 88

MRQTIKVIKFILIICTVYYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMRLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQLTKNAQDKLELHFLMMSGIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRLALHIKFTDIKEIPLWI
YSLKTEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRLALHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT
GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT
TGCTTGGGTGATTCTCGGATCTCCCCTGTTGATTTCGGTGCTCTCCTGGGGACCTTACCTGT
ACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAATAAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTTGTCTTTGTCAGCGC
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTGAGGAGGCCTG
GGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGT
ACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

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FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNBKGLYRE
ATELWGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQORDALS
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPPELPKFSQLKWKALYSDPKSLETSFVKSYSKNLAFYWILKAGHMVP
SDQGDMAKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGCGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACCTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTCGCCATCATAAACA
ACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
GTCGGCCCAATCGGCCCCGGTGTCTACACCAATATCAGCCACCACTTTGAGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCAGCCAGACCCCTCCTGGCCACTACTCTTTTTCCCTCT
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTAGGCCTACCTGAGCCCATGCAGCCTGGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTTGTGTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 92

MGARGALLLALLLARAGLRKPESQEAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSRLRLW
DSHVCVSVLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIINNSMCNHLFLKYSEFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

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FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCCTAGGGCT
CTTTGCCCTCATCTCTCTGGCAAATGCAGTTACAGCCCGGAGCCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGTCCCTGGGCGGTGCGGACCCTGAGGAAGAGCTGAGTCTCACCTTT
GCCCTGAGACAGCAGAATGTGGAAAGACTCTCGGAGCTGGTGCAGGCTGTGTGCGGATCCCAG
CTCTCCTCAATACGGAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
CACTGACCCTCCACACGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCAGAAAGTGCCATTCT
GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCTTGGCCCCCATGTGGACTTTGTGGGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGCAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGGTAACCCCTCTGTGATCCGTAAGCGATAACAATTGACCTCACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTTCTGGAGCAGTATTTCCATGAC
TCAGACCTGGCTCAGTTCATGCGCCTCTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCGGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGCTGGTGCCAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA
AACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCCTGCTCTTCGCCTCAGGTGACAGT
GGGGCCGGGTGTTGGTCTGTCTCTGGAAGACACCAGTTCCGCCCTACCTTCCTGCCTCCAG
CCCCTATGTCACCACAGTGGGAGGCACATCCTTCCAGGAACCTTTCTCATCACAATGAAA
TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCACAGGCCTTCATACCAGGAG
GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCCATTCATGGGTGTCCGGAACCTCGGCCTCTACTCCAGTGTTTGGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGCCCGCCCCCTCTTGGCTTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCCTGGCTGGGATCCTGTAACAGGC
TGGGGAACACCAACTTCCCAGCTTTGCTGAAGACTCTACTCAACCCCTGACCCTTTCTATC
AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTTCAGTCCCTTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
TGCTGTGAGCTTGACTTGACTCCCAACCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTTAGATTCTTCAATAAGATGCTGTAAGTACTGATTTTTTTGAATGCCTCTCCCTCCGC
ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTTGATATTCATTCCCCAATTCAGTGAAGGAGACCTCTACTGTCACCGTTTACTCT
TTCCTACCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTTGCTTTATG
GCCTTTCCATCATAGTTGCCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAAGTTCTCTG
ACTACTCTTGTCTTCTCTCTCATCAATTTCTGCTTCTTCATGGAATGCTGACCTTCATTGC
TCCATTTGTAGATTTTTGCTCTTCTCAGTTTACTCATTGTCCCCTGGAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAA
TGTAACAAA

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FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQQKCHSVITQDFLTCWL
SIRQAELLLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMASAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGLFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

[illegible][illegible]

FIGURE 96

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKS
RRKRQIYGYSRFSIFGKDFFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG
TQKLRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD
AQPASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCCGCCCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCCTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC
ACTGCTGCCCCACTGTTTCAAGGACAACCTGAACAAACCATACTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGGAACCCCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCCTGTGTATTCTTGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCTCAGACCCTGCAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG
CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCCCGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCCGAC
GGCCTCAGGCCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCCCGCCCCCAC
GACTTCCGGCCCCGCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTTAT
AGGTATTTGTAACCCTGCCACATATCTTATTTATTCTCCAATTTCAATAAATTATTTATT
CTCCAAAAAAAAA

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FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318

><subunit 1 of 1, 317 aa, 1 stop

><MW: 33732, pI: 7.90, NX(S/T): 1

MVVGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA
WVEPHFPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRWSVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

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FIGURE 99

GACGGCTGGCCACCAATGCACGGCTCCTGCAGTTTCTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGTATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGGCCAC
AACAAGGAGCGCGGGCGCCGCGGCGAGAATCTGTTCCGCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTTGCCTTACCTGGTAACTGAGGCCCCATCCTTCCGGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCCCTATCCCAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG
GGAACCTCTACCCCATGCCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG
AGGTCTTGGCCTCAGTTTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCCTTGCCAGGTGCAGAGGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGCTGGCTGGAATCTTCTTGAATGGGATAACCACTCAAAGGG
TGAAGAGGTCAGCTGTCTCCTGTCATCTTCCCCACCCTGTCCCCAGCCCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACC
GGGCCCACACCTCTCCTGCCCCCTCCCTCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCT
CACTGCCTACCTGGCCTGGGGCTGTCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG
TGTAGCTGGGGATGGGGATTCCCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC
TTTGAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLVYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLGVEETNIELLVLCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRAEASDSRKMGTTPSSLATGIPAFVLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVWGPLLGLLLLLPPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

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FIGURE 101

GTAAGTGAAGTCAGGCTTTTTCATTTGGGAAGCCCCCTCAACAGAATTTCGGTCATTCTCCAAGTTATGGTGGACGT
ACTTCTGTTGTTCTCCCTCTGCTTGCTTTTTTTCACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTTTCAT
CAAGGCAAGTTCCATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACTGAACAACAATGAATTGGAGACCATTCC
AAATCTGGGACCAGTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
ACATCTGAAAGAGTTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAACTGCATT
TCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCCGAGTCACATCAATGGAACCTGGGTATTTTGACAA
TTTGGCCAACACACTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCCAAGATGTTTAAACT
GCCCCAAGTGAACATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGG
TGCTCTGAAGTCTCTGAAAATGCAAAGAAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGGCTGAGCAA
CATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCT
GCAGGAACCTTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAG
TGAGCTGGACCTAACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTTGGCCTAAGCTTACTAAATAC
ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGGCTTTCCAGTTTAAAGACTTT
GGATCTGAAGAACAATGAAATTTCTTGGACTATTGAAGACATGAATGGTGTCTTCTCTGGGCTTGACAACTGAG
GCGACTGATACTCCAAGGAAATCGGATCCGTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCA
TCTAGACCTGAGTGACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAATGAAGAACTGCAACAATT
GCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCCACAGTGGGTGGCGGAAACAACCTT
TCAGAGCTTTGTAAATGCCAGTTGTGCCCCATCCTCAGCTGCTAAAAGGAAGAAGCATTTTGTCTGTTAGCCCCAGA
TGGCTTTGTGTGTGATGATTTTCCCAAACCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTT
CAATTTGAGTTTTCATCTGCTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTTTGTCTGGAAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACCAC
CATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCTCCAATCACTTTGGTTT
ATCCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCAT
CCGAGCTGGGGCCATGGCACGCTTGGAGTGTGCTGTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA
TGGGGGCACAGACTTCCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGACGTGTTCTTTATCGT
GGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTTCAGCAAATGC
AACTCTGACTGTCTTAGAAACACCATCATTTTTGCGGCCACTGTTGGACCGAAGTGAACCAAGGGAGAAACAGC
CGTCTTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTTGGTGGT
AACCGAGAGGCACTTTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTGATGCTGGGAA
ATACACATGTGAGATGTCTAACACCCTTGACACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAAC
CTGCGACTCCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCTGTGATCATAGC
CGTGGTTTGTGTGTGGTGGGCACGTCACTCGTGTGGGTGGTTCATCATATACCACACAAGGCGGAGGAATGAAGA
TTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCTCAGGGAACGTT
AGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACAGTTTGTCTCATCTTCAGGTGCTGG
ATTTTTCTTACCACAACATGACAGTAGTGGGACTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGC
CACAGATCTGTTCTTTGTCCGTTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGA
TCCTTTTGAACATATCATACAGGTTGCAGTCTTGACCCAAGAACAGTTTAAATGGACCACTATGAGCCCAGTTA
CATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATC
GTGGCCTTCACATGTGAGGAAGCTACTTAACACTAGTTACTCTCAATGAAGGACCTGGAATGAAAAATCTGTG
TCTAAACAAGTCCCTTTTAGATTTTAGTGCAAATCCAGAGCCAGCGTTCGGTTGCCTCGAGTAATTTCTTTCATGGG
TACCTTTGGAAAAGCTCTCAGGAGACCTCAGCTAGATGCCTATTCAAGCTTTGGACAGCCATCAGATTGTCAGCC
AAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAAGAAAGGAC
AGATTTTCAGGAAGAAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACACAGGACTCCAAATTTTCAGTC
TTATGACTTGGACACATAGACTGAATGAGACCAAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATTTA
AAAGAGAGAGAATCTTATGTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAATGCTTTATTTATACAGAT
GAACCAAAATTACAAAAGTTATGAAAATTTTATACTGGGAATGATGCTCATATAAGAATACCTTTTAAACTA
TTTTTTAACTTTGTTTTATGCAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTT
TTATAATGCCAGATTTCTTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCTTGTACCATTTT
TTAAATAGAAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAA

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FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRI SAIPPKMFKL PQLOHLELNRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE
FCQKLSELDLTFNHL SRLDDSSFLGLSLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWLPQWVAENNFSQSFVNASCAHPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETSPFLRPLLDRTVTKGETAVLQCIAGGSPPPKNLWTKDDSPLVVTER
HFFAAGNQLLIIVDSVDVSDAGKYTCEMSNTLGTGERGNVRLSVIPTPTCDSPQMTAPSLDDDG
WATVGVV IIAVCCVVGTSLVWVVI IYHTRRRNEDCSITNTDETNPADIPSYLSSQGTLD
RQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDPFETYHTGCSPPDPTVLMHDHYEPSYIKKKECYPCSHPSEESCERSFSNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTLNRYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

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SECRET

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGI STNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNPNIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDLDELDSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNCDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASLTLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVSNSVGN
TTASATLNVTAATTTTFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKFTTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

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FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTTCCCTCCTGCTGTTTGGGGGCA
TGAAAGGGCTTCGCCGCCCGGAGTAAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGAGCGCGCACGCGACCGC
GAGGGCGGGCGTGCACCCCTCGGCTGGAAGTTTGTGCCGGGCCCCGAGCGCGCGCGGGCTGGGAGCTTCGGGTAGA
GACCTAGGGCCGTGGACCGCGATGAGCGCGCGGAGCCTCCGTGCGCGCGCGCGGGGTGGGGCTGCTGCTGTGC
GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGCGCGGTCCGCGGGGAACCTCGGGCAGCCCTCTGGGGTAGCCGCC
GAGCGCCCATGCCCCACTACCTGCCGCTGCCTCGGGGACCTGCTGGACTGCAGTCGTAAGCGGCTAGCGCGCTTT
CCCGAGCCACTCCCGTCTGGGTGCTCGGCTGGACTTAAGTCACAACAGATTATCTTTTCATCAAGGCAAGTTCC
ATGAGCCACCTTCAAAGCCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA
GTCTCGGCAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTTGAACTTTGGACCTTAGCAGCAACAATATTTAGAGCTCCAACTGCATTTCCAGCCCTACAG
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACA
CTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCAAGATGTTTAAACTGCCCCAATCGCAA
CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGGTGCTCTGAAGTCT
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTTTGGGGGCTGAGCAACATGGAAATTTTG
CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTCAT
CTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCCTAAGCTTACTAAATACACTGCACATTGGG
AACAACAGAGTCAGCTACATTGCTGATTGTGCCTTCCGGGGCTTCCAGTTTAAAGACTTTGGATCTGAAGAAC
AATGAAATTTCTGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCAAAATGAAGAAACTGCAACAATTGCATTTAAATACA
TCAAGCCTTTTGTGCGATTGCCAGCTAAATGGCTCCACAGTGGGTGGCGGAAAAACAACCTTTCAGAGCTTTGTA
AATGCCAGTTGTGCCCATCTCAGCTGCTAAAAGGAAGAAGCATTTTGTGTTAGCCAGATGGCTTTGTGTGT
GATGATTTTCCCAAACCCAGATCACGGTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC
ATCTGCTCAGCTGCCAGCAGCAGTGAATCCCCAATGACTTTTGTCTGGAAAAAGACAATGAACTACTGCATGAT
GCTGAAATGGAAATTTATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACCACCATCCTTCGGCTG
CGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCTCAATCACTTTGGTTTCATCCTACTCTGTC
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGGCC
ATGGCAGCTTGGAGTGTGCTGCTGTGGGGCACCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGGCACAGAC
TTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGACGTGTTCTTTATCGTGGATGTGAAGATA
GAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTAGCAAATGCAACTCTGACTGTC
CTAGAAACACCATCATTTTTTGGCGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAACTGAACCTGGACCAAAGATGATAGCCCATTTGGTGGTAACCGAGAGGCAC
TTTTTTGAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTGATGCTGGGAAATACACATGCTGGAG
ATGTCTAACACCCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAACCTGCCACTCCCT
CAGATGACAGCCCCATCGTTAGACGATGACGGATGGGGCACTGTGGGTGTCTGATCATAGCCGTGGTTTTGCTGT
GTGGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTACC
AACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCTCATCTCAGGGAACGTTAGCTGACAGGCAG
GATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACAGTTTGTGCATCTTCAGGTGCTGGATTTTTCTTACCA
CAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTC
CTTTGTCCGTTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAATGTGTATGGCTCAGATCCTTTTGAACA
TATCATACAGGTTGCAGTCTTGACCCAAGAACAGTTTTAATGGACCACTATGAGCCCAGTTACATAAAGAAAAAG
GAGTGCTACCCATGTTCTCATCCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACAT
GTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC
TCTTTAGATTTTAGTGCAATCCAGAGCCAGCGTCGGTTGCCTCGAGTAATTTCTTCATGGGTACCTTTGGAAAA
GCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCAGATTGTGAGCCAAGAGCCTTTTAT
TTGAAAGCTCATCTTCCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAA
GAAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC
ACATAGACTGAATGAGACCAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTATTTAAAGAGAGAGAAT
CTTATGTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAATGCTTTATTTATACAGATGAACCAAATTAAC
AAAAAGTTATGAAAATTTTATACTGGGAATGATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTG
TTTTATGCAAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTTTATAATGCCAGA
TTTCTTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATTAATACCTGCCTTGTACCATTTTTTAAATAGAAGTT
ACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAAAAA

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FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLLDCSR
 KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT
 LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
 FDNLANITLLVLKLNRRNRI SAIPPKMFKL PQLOHLELNRNKIKNVDGLTFQGLGALKSLKMQR
 NGVTKLMDGAFWGLSNMEILQLDHNNTL EITKGWLYGLLMLQELHLSQNAINRISPDAWEFC
 QKLSELDLTFNHL SRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNEIS
 WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSOMK
 KLQQLHLNTSSLLCDCQLKWL PQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDFF
 PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENY AHLRAQGGGE
 VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA
 RLECAAVGHPAPQIAWQKDG GTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
 GSISANATLTVLETSPFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTERHF
 FAAGNQLLIIVDSVDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDDGWA
 TVGVVVI IAVVCCVVGTSLVWVVI IYHTRRRNEDCSITNTDETNPADIPSYLSSQGT LADRQ
 DGYVSSESGSHHQFVTSSGAGFFLPQH DSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
 LKGNVYGSDPFETYHTGCSPDPRTVLMDHYEPSYIKKKECYPCSHPSEESCERSFSNISWPS
 HVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDAYS
 SFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FOOTNOTES: 071801 0000000000

FIGURE 107

CAAACTTGCCTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCAGCTGAGAC
TGGGGGAGCGCGTTTCGGCCTGTGGGGCGCCGCTCGGCGCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCTGGGTGGTCCCGTCCCCCTATCCCTCCTTTATATA
GAAACCTTCCACACTGGGAAGGCAGCGGCGAGGCAGGAGGGCTCATGGTGAAGGAGGCGGCTGATCTGCAG
GCGCACAGCATTCGAGTTTACAGATTTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACAGCCTGCCTGGT
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCCAGAGCCGGGTGCTGC
TGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGCCGTGAGGGCCCCAGGATTTGGCCGAA
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTTGCGGAGGAGGAGCCGGTGTGCTGGTACTGAGCCCTGAGG
AGCCCGGGCCTGGCCCAGCCGCGGTGAGCTGCCCCCGAGACTGTGCTGTTCCAGGAGGGCGTCTGAGACTGTG
GCGGTATTGACCTGCGTGAGTTCCCGGGGACCTGCCTGAGCACACCAACACCTATCTCTGCAGAACCAACAGC
TGGAAGATCTACCTGAGGAGCTCTCCGGCTGCACCGCTGGAGACACTGAACCTGCAAAACAACCGCCTGA
CTTCCCGAGGGCTCCAGAGAAGGCGTTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC
TGACCTTGGCACCCCGCTTCTGCCAAACGCCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAGATCT
ATGGGCTCACCTTTGGCCAGAAGCCAACTTGAGGTCTGTGTACCTGCACAACAACAAGCTGGCAGACGCCGGGC
TGCCGGACAACATGTTCAACGGCTCCAGCAACGTGAGGTCTCATCTGTCCAGCAACTTCTGCGCCACGTGC
CCAAGCACCTGCCGCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTGGAGAAGATCCCCCGGGGGCCT
TCAGCGAGCTGAGCAGCTGCGGAGCTATACCTGCAGAACAACTACCTGACTGACGAGGGCCTGGACAACGAGA
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCCAGCTGGGCTGC
CGCGCAGCCTGGTGTGCTGCACTTGGAAGAAGACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGCTGCACAGCAACAGCTGCGGGAGCAGGGCATCCACCCACTGGCCTTCCAGGGCC
TCAAGCGGTGCAACACGGTGCACCTGTACAACAACCGCTGGAGCGCGTGCACAGTGGCCTGCCTCGCCGCGTGC
GCACCTCATGATCTGCACAACAGATCAAGGCATTGGCCGCGAAGACTTTGCCACCACCTACTTCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACCAGCCACAGGTGCACCGCAGCGCTTCCGCAAGCTGCGCCTGCTGC
GCTCGCTGGACCTGTGCGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCTCGAAATGTCCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCCTTGGCACGAGGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCCGTGCCTGGGTGGACCTCGCCCATCTGCAGCTGCTGGACA
TCGCGGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGAGTACCTGTACCTGCAGAACACA
AGATTAGTGCGGTGGCCGCAATGCCTTCGACTCCACGCCCAACCTCAAGGGGATCTTTCTCAGGTTTAACAAGC
TGGCTGTGGGCTCCGTGGTGACAGTGCCCTTCGGGAGGCTGAAGCACCTGCAGGTCTTGACATTGAAGGCACT
TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGACTCTTTTCTGC
AGCACACGCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA
TCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCCACGGCGTGTCCACGGCCAGACACATGC
ACACACATCACACCTCAAACACCCAGCTCAGCCACACACAACCTACCTCCAAACCACACAGTCTCTGTACAC
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAGGGTCTGCCCCCTGCCCTGGCACACACAGGCACCCA
TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACCACACACACATGCACAAGTCATGTGCGAA
CAGCCCTCAAAGCCTATGCCACAGACAGCTCTTGCCCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCT
GTCCATCTGTCCGTCCGTTCCCTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCTCT
GGAACCTCAAAAAGCTGGCTTTTATTCTTTCCCATCTATGGGGACAGGAGCCTTCAGGACTGCTGGCCTGGCC
TGGCCACCCCTGCTCCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCATTTTCCAATGGGCAAGCCCAGTGGAGGCAGGATGGGAGAGCCCCCTGGGTGCTGCTGGGGCCTTGGGG
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTTT
GTTCTTCAGGCCTGTGGGGGAAGTTCCGGGTGCCTTTATTTTATTCTTTTCTAAGGAAAAAATGATAAAAT
CTCAAAGCTGATTTTCTTGTATAGAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPWPGRPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPEENEFAEEEPVLVLSPPEPGPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP
EHTNHLSTLQNNQLEKIYPEELSRHLRLETNLQNNRLTSRGLPEKAFFEHLTNLNYLYLANNK
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMLHNQITGIGREDFATTYF
LEELNLSYNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

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FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTCTCCGGGAGCGGCAG
CAGTAGCCCGGGCGGCGAGGGCTGGGGGTTTCCTCGAGACTCTCAGAGGGGCGCCTCCCATCGGCGCCACCACCC
CAACCTGTTCTCGCGCGCCACTGCGCTGCGCCCCAGGACCCGCTGCCCAACATGGATTTTCTCCTGGCGCTGGT
GCTGGTATCCTCGCTCTACCTGCAGGCGGCCGCGAGTTCGACGGGAGGTGGCCAGGCAAATAGTGTATCGAT
TGGCCTATGTCGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTAGCC
TGTGTGCCAACACGATGCAAAACATGGTGAATGTATCGGGCCAAACAAGTGCAAGTGTATCCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAGCACAGGTGCATGAACACTTA
CGGCAGCTACAAGTGCTACTGTCTCAACGGATATATGCTCATGCCGGATGGTTCTGCTCAAGTGCCCTGACCTG
CTCCATGGCAAACCTGTAGTATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCCTGGCCT
GCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCCTGCCCTAGATT
TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTCTAAAGGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTGTCTCGATGTTATAA
CGTACGTGGGTCTTACAAGTGCAAATGTAAAGAAGGATACCAGGGTGATGGACTGACTTGTGTGTATATCCCAA
AGTTATGATTGAACCTTCAGGTCCAATTCATGTACCAAAGGGAAATGGTACCATTTTAAAGGGTGACACAGGAAA
TAATAATTGGATTCTGATGTTGGAAGTACTTGGTGGCCTCCGAAGACACCATATATTCCTCCTATCATTACCAA
CAGGCCTACTTCTAAGCCAACAACAAGACCTACACCAAAGCCAACACCAATTCCTACTCCACCACCACCACCACC
CCTGCCAACAGAGCTCAGAACACCTTACCACCTACAACCCAGAAAGGCCAACACCGGACTGACAACCTATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACCTTCAGAAACCCAGAGG
AGATGTGTTTCACTGTTCTGGTACACAGTTGTAATTTTGACCATGGACTTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGCAGCCAAAGCCCCAGG
GGGAAAAGCTGCACGCTTGGTGCTACCTCTCGGCCGCTCATGCATTAGGGGACCTGTGCCTGTCAATTCAGGCA
CAAGGTGACGGGGCTGCACTCTGGCACACTCCAGGTGTTTGTGAGAAAACACGGTGCCACGGAGCAGCCCTGTG
GGGAAGAAATGGTGGCCATGGCTGGAGGCAAACACAGATCACCTTGCAGGGGGCTGACATCAAGAGCGAATCACA
AAGATGATTTAAAGGGTTGGAAAAAAGATCTATGATGGAAAATTAAGGAACTGGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGGCAAACCATTTGATGGTTTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCGACCAGCTG
TTCTCCATATGCACTAAGAATAGAACAAGAGGAACTGGCTTAGACTAGAGTATAAGGGAGCATTTCCTTGGCAGG
GGCCATTGTTAGAATACTTCATAAAAAAAGAGTGTGAAAATCTCAGTATCTCTCTCTTTCTAAAAAATTAGA
TAAAAATTTGTCTATTTAAGATGGTTAAAGATGTTCTTACCCAAGGAAAAGTAACAAATTATAGAATTTCCCAA
AGATGTTTTGATCCTACTAGTAGTATGCAGTGAAAATCTTTAGAACTAAATAATTTGGACAAGGCCTTAATTTAGG
CATTTCCCTCTTGACCTCCTAATGGAGAGGGATTGAAAGGGGAAGAGCCCACCAAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCCTAGCAGTATTAAAGAAAAAAGGAACTATTTATTCCAAATGAGAGTATGATGGAC
AGATATTTTAGTATCTCAGTAATGTCCTAGTGTGGCGGTGGTTTTCAATGTTTCTTCATGGTAAAGGTATAAGCC
TTTCATTTGTTCAATGGATGATGTTTCAGATTTTTTTTTTTTTTAAGAGATCCTTCAAGGAACACAGTTCAGAGAG
ATTTTCATCGGGTGCACTCTCTCTGCTTCGTGTGTGACAAGTTATCTTGGCTGCTGAGAAAGAGTGCCCTGCCCC
ACACCGGCAGACCTTTCTTTCACCTCATCAGTATGATTCAGTTTCTTATCAATTGGACTCTCCAGGTTCCAC
AGAACAGTAATATTTTTTGAACAATAGGTACAATAGAAGTCTTCTGTCAATTAACCTGGTAAAGGCAGGGCTGG
AGGGGGAAAAATAAATCATTAAGCCTTTGAGTAACGGCAGAATATATGGCTGTAGATCCATTTTTTAATGGTTTATT
TCCTTTATGGTCAATAACTGCACAGCTGAAGATGAAAGGGGAAAAATAAATGAAAATTTTACTTTTCGATGCCAA
TGATACATTGCACATAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTTGTATTATTATTAATGTTTT
CTAAAATAAAAAATGTTAGTGGTTTTCCAAATGGCCTAATAAAAAACAATTATTTGTAAATAAAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGEICIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGC DVVKQI RCQCPS PGLHLAPDGRTCVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDEC SLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGN GTILKGD TGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDN
RVQTD PQKPRGDVFSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAAKAPGG
KAARLVLP LGR LMHSGDLCL SFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

090920" 02E60660

| | 0 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| 0 | 00000000 | 00000001 | 00000010 | 00000011 | 00000100 | 00000101 | 00000110 | 00000111 | 00001000 | 00001001 | 00001010 | 00001011 | 00001100 | 00001101 | 00001110 | 00001111 | 00010000 | 00010001 | 00010010 | 00010011 | 00010100 | 00010101 | 00010110 | 00010111 | 00011000 | 00011001 | 00011010 | 00011011 | 00011100 | 00011101 | 00011110 | 00011111 | 00100000 | 00100001 | 00100010 | 00100011 | 00100100 | 00100101 | 00100110 | 00100111 | 00101000 | 00101001 | 00101010 | 00101011 | 00101100 | 00101101 | 00101110 | 00101111 | 00110000 | 00110001 | 00110010 | 00110011 | 00110100 | 00110101 | 00110110 | 00110111 | 00111000 | 00111001 | 00111010 | 00111011 | 00111100 | 00111101 | 00111110 | 00111111 | 01000000 | 01000001 | 01000010 | 01000011 | 01000100 | 01000101 | 01000110 | 01000111 | 01001000 | 01001001 | 01001010 | 01001011 | 01001100 | 01001101 | 01001110 | 01001111 | 01010000 | 01010001 | 01010010 | 01010011 | 01010100 | 01010101 | 01010110 | 01010111 | 01011000 | 01011001 | 01011010 | 01011011 | 01011100 | 01011101 | 01011110 | 01011111 | 01100000 | 01100001 | 01100010 | 01100011 | 01100100 | 01100101 | 01100110 | 01100111 | 01101000 | 01101001 | 01101010 | 01101011 | 01101100 | 01101101 | 01101110 | 01101111 | 01110000 | 01110001 | 01110010 | 01110011 | 01110100 | 01110101 | 01110110 | 01110111 | 01111000 | 01111001 | 01111010 | 01111011 | 01111100 | 01111101 | 01111110 | 01111111 | 10000000 | 10000001 | 10000010 | 10000011 | 10000100 | 10000101 | 10000110 | 10000111 | 10001000 | 10001001 | 10001010 | 10001011 | 10001100 | 10001101 | 10001110 | 10001111 | 10010000 | 10010001 | 10010010 | 10010011 | 10010100 | 10010101 | 10010110 | 10010111 | 10011000 | 10011001 | 10011010 | 10011011 | 10011100 | 10011101 | 10011110 | 10011111 | 10100000 | 10100001 | 10100010 | 10100011 | 10100100 | 10100101 | 10100110 | 10100111 | 10101000 | 10101001 | 10101010 | 10101011 | 10101100 | 10101101 | 10101110 | 10101111 | 10110000 | 10110001 | 10110010 | 10110011 | 10110100 | 10110101 | 10110110 | 10110111 | 10111000 | 10111001 | 10111010 | 10111011 | 10111100 | 10111101 | 10111110 | 10111111 | 11000000 | 11000001 | 11000010 | 11000011 | 11000100 | 11000101 | 11000110 | 11000111 | 11001000 | 11001001 | 11001010 | 11001011 | 11001100 | 11001101 | 11001110 | 11001111 | 11010000 | 11010001 | 11010010 | 11010011 | 11010100 | 11010101 | 11010110 | 11010111 | 11011000 | 11011001 | 11011010 | 11011011 | 11011100 | 11011101 | 11011110 | 11011111 | 11100000 | 11100001 | 11100010 | 11100011 | 11100100 | 11100101 | 11100110 | 11100111 | 11101000 | 11101001 | 11101010 | 11101011 | 11101100 | 11101101 | 11101110 | 11101111 | 11110000 | 11110001 | 11110010 | 11110011 | 11110100 | 11110101 | 11110110 | 11110111 | 11111000 | 11111001 | 11111010 | 11111011 | 11111100 | 11111101 | 11111110 | 11111111 |

CTTCTTTTGA AAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCCCTTTAGATTGTGA
AAATGTGGCTCAAGGTCCTTCAACAACCTTTCCCTTTTGCAACAGGTGCTTGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA
CACAAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCCTGACTTGGAATACC
AACACAAGTTCCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTT
GATGAAGGCAATTACATCGTGAAGGTCAACATTTCAGGGAAATGGAACCTATCTGCCAGTCA
GAAGATACAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTTCCTCCTT
CTGGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
TCCCCAAAACAATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCTGGTGAGGAACCTGTGAGTGAATCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT
TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGGCTCGCTTAGAAGTT
GCATCTGAGAAAAGTAGCCAGAAAGACAATGGACTATGTGTGCTGTGCTTACAACAATAAC
CGGCAGGCAAGATGAAACTCATTTACAGTTATCATCACTTCGCTAGGACTGGAGAAGCTTG
CACAGAAAAGGAAAATCATTGTACCTTTAGCAAGTATAACTGGAATATCACTATTTTTGATT
ATATCCATGTGTCTTCTCTTCTATGGAAAAAATATCAACCCTACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT
GTATGAAGTTATTCAGCACATCCCTGCCCAGCAGCAAGACCATCCAGAGTGAACTTTCATGG
GCTAAACAGTACATTTCGAGTGAAATTCTGAAGAAACATTTTAAAGGAAAAACAGTGGAAGT
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCCTTTACA
TGCAGAATAGAGGCATTTATGCAAATTGAACTGCAGGTTTTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGGAAATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGGTTTCTCATAAGTTTTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACACTTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAAACTTTACATTGTTTCGATTTTTTCAGCAGACTTTGTTTTATTAAATTTTTATTAGTG
TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTTATTTGTACAA
CAAAGTAATAAGGATGGTTGTCAAAAAACAAAATATGCCTTCTCTTTTTTTTTCAATCACC
AGTAGTATTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTTA
TTTTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTTTGGCTTTTAAAAAAAAAAAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTSLASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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TOTAL 20 "09909320

FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTGCAAGTTCCCCTGGCAGTCCTGGTGCTGTT
GCTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCT
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTTGCTGAATGGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC
TTCCTACTATTTATCATTTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTTATAAGTGATAAAGAGTGGAAGAGTATTGAGCCCGTTTTATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT
GTTTTTGCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC
AGATTGCCTTTGTCTTCAAAAAGGCGCAGACCACAGCCATACCATAACCCTTCAAAAAAAT
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAGACTTTCCACAGAATGC
CATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAATCCTAGTTAAATTTTATAG
TTATCTTAATATTATGATTTTGATAAAAACAGAAGATTGATCATTTTGTTTGGTTTGAAGTG
AACTGTGACTTTTTTTGAATATTGCAGGGTTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTATACAAGTTTGAAATATGATTTAAGCACAGTATGATG
GTTTAAATAGTTCTCTAATTTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTTGT
TTAATAATAACCTATTTCAAGTCTGAGTTTTGAAATTTACATTTCCCAAGTATTGCATTAT
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTCTCTG
TTTCACTGTGTGAAAAAAGAAGATATTTCCCATAAATGGGAAGTTTGCCCATTTGTCTCAAG
AAATGTGTATTTTCACTGACAATTTTCGTGGTCTTTTTTAGAGGTATATTCAAAATTTCTTGT
ATTTTTAGGTTATGCAACTAATAAAAACTACCTTACATTAATTAATTACAGTTTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTTAAGTTCATGGTATTTCTCTTGATTC
CAACAAAGTTTGATTTTTCTCTTGATTTTTTCTTACTTACTATGGGTACATTTTTTTATTTTT
CAAATTGGATGATAATTTCTTGGAACATTTTTTATGTTTTTAGTAAACAGTATTTTTTTTGT
GTTTCAAACCTGAAGTTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTTAAATTT
TTGGCCACTTTTTTTCAGATTTTACATCATTTCTTGCTGAACCTTCAACTTGAAATTGTTTTTT
TTTCTTTTTTGATGTGAAGGTGAACATTCCTGATTTTTTGTCTGATGTGAAAAGCCTTGGA
TTTTACATTTTGAAAATTCAAAGAAGCTTAATATAAAAAGTTTGCATTCTACTCAGGAAAAAG
CATCTTCTTGATATATGTCTTAAATGTATTTTTTGTCTCATATACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTTGATGTTTTTAAAATAATAACATTTTTTATATTTTTTAAAGACAA
ACTTCATATTATCCTGTGTTCTTTCTGACTGGTAATATTGTGTGGGATTTTACAGGTAATA
GTCAGTAGGATGGAACATTTTAGTGATTTTTTACTCCTTAAAGAGCTAGAATACATAGTTTT
CACCTTAAAAGAAGGGGGAAAAATCATAAATACAATGAATCAACTGACCATTACGTAGTAGAC
AATTTCTGTAATGTCCCCTTCTTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTTACAG
TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAATATTGTACCATT
AAAGAGTTTGGATGTGTAACCTGTGATGCCTTAGAAAAATATCCTAAGCACAAAATAAACCT
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAAAAAAAA

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FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEEQEAEDEEDVSE
EEAESKEGTNKDFPQNAIRQPSLGPSTLTDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

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FIGURE 115

CGGAGTGTCCAGCTGCGGAGACCCGTGATAATTTCGTAACTAATTCAACAAACGGGACCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCAGTGGGACAGGCGGATTGGAAGAGCGGG
AAGGTCTTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC
ATTGCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGCAGGCCGAATTCTTCACCTCTATTG
GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAACTGG
TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
GGTTTTATCGCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGG
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA
GAGGGGAACCTTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG
GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCCTGCTC
TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACGTAAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCA
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGGG
GAGGGTGTCAAACCTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA
CAGGGCCCCACAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA
TCGTCAGGTACTACGATGTCTGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CCTAAACTTGCACGAGCCACCGTTTCGTGATCCCAAGACAGGAGTCCTCACTGTCGCCAGCTA
CCGGGTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCCTGTTGTGGCCCGAGTAAATC
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT
TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGG
CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGTGTAGAAGCTG
GTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTTGCAGGAGCGGGGAAGGTGACTACCGAACAAGACATGCTGCCTGCCC
TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAAGTTGACTGAATCCTTTTCTGTCCTTCCCCCTTCTGTGTC
CTTCAGCCCATGTCAACGTGACAGACACCTTTGTATGTTTCTTTGTATGTTTCTATCAGGCT
GATTTTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCCAGCCCTTCCATTCAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTTCAGTGAACCAAAGTTCTGATACCTTGTTTACATGTTTGTTTTTAT
GGCATTTCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAGAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYA EKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPAL EDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGA AKALMRLQDTYRLDPGTISR GELPGTKYQAMLSVDDCFGMGRSAYNEG DYYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEEREKTLTNQTEAELATPEGIYERPVDYLP ERDVYESLCRGE GVKLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDDPVVARVNR RMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRS GEGDYR
TRHAACPVLVGCKWVSNKWFHERGQEF LRPCGST EVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTTACTTCCTCCTCTTTTTTAGTGGAAGACAGACCATAATCCCAGTGTGAGTGAAATTGATTGT
TTCATTTATTACCGTTTTGGCTGGGGGTAGTTCCGACACCTTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTTCTTGGGGATGCTGGTCCCTGGAAGCCAGCGGGCCTTGCTCTGTCTTTGGCCTCATTGACCC
CAGGTTCTCTGGTTAAACTGAAAGCCTACTACTGGCCTGGTGCCCATCAATCCATTGATCCTTGAGGCTGTGCC
CCTGGGGCACCCACCTGGCAGGGCCTACCACCATGCGACTGAGCTCCCTGTTGGCTCTGCTGCGGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCTCTGGGGTGACGCTGAGCCTCCTGCGGGTTTCTTGATCCAGGGGGAGGGAGAAG
ATCCCTGTGTGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG
ATGAAGACTTCAAACCCCGGATTGTCCCCTACTACAGGGACCCCAACAAGCCCTACAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGGCTCCCGTGAGCGGTTGCTGGTGGCTGTCTGACCTCCCGAGCTACACTGTCCA
CTTTGGCCGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCCTCGGTTACTCTACTTCACTGGGCAGCGGGGG
CCCGGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGGATGAGCGGGCCCGCTGGCTCATGTCAGAGACCCTGC
GCCACCTTCACACACACTTTGGGGCCGACTACGACTGGTTCTTCATCATGCAGGATGACACATATGTGCAGGCCC
CCCGCTGGCAGCCCTTGCTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGGCAGAGGAGTTTCATTG
GCGCAGGCGAGCAGGCCCGGTACTGTCTATGGGGGCTTTGGCTACCTGTTGTACGGAGTCTCCTGCTTCGTCTGC
GGCCACATCTGGATGGCTGCCGAGGAGACATTTCTAGTGCCCGTCTGACGAGTGGCTTGACGCTGCCTCATTG
ACTCTCTGGGCGTCGGCTGTGTCTCAGCACCAGGGGCGAGCAGTATCGCTCATTTGAACTGGCCAAAAATAGGG
ACCCTGAGAAGGAAGGGAGCTCGGCTTCTGAGTGCCTTCGCCGTGCACCCTGTCTCCGAAGGTACCTCATGT
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAATAGAACAACTGCAGGCTCAGA
TCCGGAACCTGACCGTGCTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCGTTGGGCTCCCTGCTCCTTTCA
CACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGCACACCTTCTCCTGTGCAGATGGGG
CTCCCAAGTGCCCACTACAGGGGGCTAGCAGGGCGGACGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGGCGCTATCAGCCCCGCTGCGCTTCCAGAAGCAGCGACTGCTCAACGGCTATCGGCGCTTCGACCCAGCAC
GGGCGATGGAGTACACCCTGGACCTGCTGTTGGAATGTGTGACACAGCGTGGGCACCGGCGGGCCCTGGCTCGCA
GGTTCAGCCTGCTGCGGCCACTGAGCCGGGTGGAATCCTACCTATGCCCTATGTCACTGAGGCCACCCGAGTGC
AGCTGGTGTGCTGCCACTCCTGGTGGCTGAAGCTGCTGACGCCCCGGCTTTCTCGAGGCGTTTGCAGCCAATGTCC
TGGAGCCACGAGAACATGCATTGCTCACCCTGTTGCTGGTCTACGGGCCACGAGAAGGTGGCCGTGGAGCTCCAG
ACCCATTTCTTGGGGTGAAGGCTGCAGCAGCGGAGTTAGAGCGACGGTACCCTGGGACGAGGCTGGCCTGGCTCG
CTGTGCGAGCAGAGGCCCTTCCCAGGTGCGACTCATGGACGTGGTCTCGAAGAAGCACCTGTGGACACTCTCT
TCTTCCTTACCACCGTGTGGAACAAGGCCTGGGCCCCGAAGTCTCAACCGCTGTGCGATGAATGCCATCTCTGGCT
GGCAGGCCTTCTTTCCAGTCCATTTCCAGGAGTTCAATCCTGCCCTGTCAACACAGAGATCACCCCAGGGCCCC
CGGGGGCTGGCCCTGACCCCCCTCCCTCCTGGTGCTGACCCCTCCCGGGGGCTCCTATAGGGGGGAGATTTG
ACCGGCAGGCTTCTGCGGAGGGCTGCTTCTACAACGCTGACTACCTGGCGGGCCGAGCCCGGTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGGCTGGAGGTGATGGATGTTTTCTCCGGTTCTCAGGGCTCC
ACCTCTTTCGGGCCGTAGAGCCAGGGCTGGTGCAAGTTCTCCCTGCGAGACTGCAGCCACGGCTCAGTGAAG
AACTCTACCACCGTGCCTCCTCAGCAACCTGGAGGGGCTAGGGGGCCGTGCCAGCTGGCTATGGCTCTCTTTG
AGCAGGAGCAGGCCAATAGCACTTAGCCCCCTGGGGGCCCTAACCTCATTACCTTTCTTTGTCTGCCCTCAGCC
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTGCTGTATTTTTTAAATATGAAAATGTTATTAA
ACATGTCTTCTGCC

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FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
QSDDEFKPRIVPYRDPNKPYPKKVLRTRYIQTELGSRRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDFFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGAPKCPLOQASRADVGDALETALEQLNRRYQPRLRFOKQRLNNGYR
RFDPARMEYTLDDLLECVTQRGHRRALARVSLRPLSRVEILPMPYVTEATRVQLVLPPL
VAEAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLNRCRMNAISGWQAFFP
VHFQEFNPALSPQRSPPGPPGAGDPDPPSPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEEALEGLEVMDFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRAQLAMALFEQEANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAACC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG
AGTTCTTCAGTTCTGAAAATGTTAAAGTGTTTGAGTCAATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACTG
GTTCTTCCTTGCACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTTGTAA
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGCTCCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTGTTTCAGATATGGCTGTTACTTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGATGATGGGGTATACCGCCTTAGGGCATTTGGGCATATTTTCAAT
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACATACATATCCAA
TACAGCTGTATGTTTCTTTTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTTTTAAATGAGGGTGGTTTTTTTCTTTAAACACATGAACATTGTAAATG
TGTTGGAAAGAAGTGTTTTAAGAATAATAATTTTGCAAATAAACTATTAATAAATATTATAT
GTGATAAATTTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTTTGCTGATTGGTT
AAAAAATTTTAACAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACCTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTTGCCTTCTCAAATGTACAACCTAAGCAACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAAT

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FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAI IENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

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FIGURE 121

CCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAGAAACAAAAAACCAAAGAGAGAGAGAAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTTCGCAT
CTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTACAGAGCTCTCCTGCT
ACAATTATGGATCAGGTTCAAGTCAAGAAATTGTTGTCCATTGAACTGGGAATATTTTCAATCC
AGCTGCTACTTCTTTTCTACTGACACCATTTCTGGGCGTTAAGTTTAAAGAACTGCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCCTACAAGA
AACCTAAATGAGAGAGTTTTTTTATTGGACTGTCAGACCAGGTTGTCGAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA
CATAGCTACCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAAATTGGA
ATGATGTAACCTGTTTCCTCAATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTG
AACAAAGGAAAATCTCTTTTAGAACAGAAGGCACAACCTCAAATGTGTAAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTTGTGCGCTGAACTTCAAAGGACTTC
ATAAGTATTTGTTACTCTGATACAAATAAAAATAAGTAGTTTTAAATGTTAAAAAAAAAAAAA
AAA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSQMFLLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDCATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

09909320 02E60660

FIGURE 123

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCTCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCCAAGTGGTACAGGAATTTGAAAGTGTGGAAGTGTCTTGCAATCATTACGGATTTCGC
AGACAAGTGACCCCAAGATCGAGTGGAAAGAAAATTCAGATGAACAAACCATATGTGTTTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGTTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTTATCGCTGTGAGGTTCGTTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT
CCAGAGCCAATCCAGATTTTCGCAATTCCTTTCCTTCCACTTAAACTCTGAAACAGGCCTTTGGTGTTCCTGCTG
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGGTTGTCTTGTCTGACTGGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAACAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTTCATCGTTTG
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTTCGTTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAGAATTTTCTCTCAAGATGGACCCGGTAAATATAACCACAA
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCCTAATCTGTTTCTGGCCTGATTCCCGCATGAGTATTAGG
GTGATCTTAAAGAGTTTGGCTCAGTAAACGCCCCGTGCTGGGCCCTGTGAAGCCAGCATGTTCACTACTGGTTCGTT
CAGCAGCCACGACAGCACCATTGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGCGGGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCTTACTTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC
TGATCGGTGTTGCAGTGTCCATTGTGGAGAAGCTTTTGGATCAGCATTGTTGTAACAAACCAAAATCAGGAAG
GTAAATTTGGTTGCTGGAAGAGGGATCTTGCTTGAGGAACCCCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAAA
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTGTTATTTTATAAAATTT
TACATCTAAATTTTGGCTAAGGATGATTTTGTATTATGAAAAGAAAATTTCTATTTAACTGTAAATATATTGT
CATACAATGTTAAATAACCTATTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTAAAT
TGGAATATCAATAATTAAGAGTATTTTACCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTTTTCT
CACACAAGTTTGTAGCCTTTTTCACAAGGGAACCTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAAATTCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAGAAACCTCTCAGGTAGCTTTGAACT
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG
CCAGTCAGTCTCTGGGGTTTGCAGGCGCCCCGCTCTAGCTACTGTTGCGCTGCTGTGCTGCCAGGAGGCCCT
GCCATCCTTGGGCCCCTGGCAGTGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTAAACAGACCTCT
TTTTGGTTATGGATGGCTCAGAAAATAGGGCCCCCAATGCTATTTTTTTTTTTAAGTTTGTGTTAATTATTTGTT
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTAAAAAGAAAATGGAT
CCCACTGTTCTCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTGAGGTGGAGCAGCCAGGTGAAAGGCCCTGGCGGGGAGGAAAG
TGAAACGCCCTGAATCAAAGCAGTTTTCTAATTTTGACTTTAAATTTTTCATCCGCCGGAGACACTGCTCCCAT
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGCTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCTGGA
GAATGGCTCTCACTACTCACCTTGTCTTTTTCAGCTTCCAGTGTCTTGGGTTTTTTTATACTTTGACAGCTTTTTTTT
AATTGCATACATGAGACTGTGTTGACTTTTTTTTAGTTATGTGAAACACTTTGCCGCGAGGCCGCTGGCAGAGGCA
GGAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCCTCAGCGTTGGGGATTACGCTCCAGCCTCCT
TCTTGGTTGTATAGTATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCCTAAACCTTCTACACTAGTGCCA
TGGGAACCAAGTCTGAAAAAGTAGAGAGAAGTGAAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTGTACTAACACACCGTAATTTGGCATTTGTTTAAAC
CTCATTATATAAAGCTTCAAAAAAACCA

090920 "026660

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTS�KIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTVPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDNLNIGGIIGG
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

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